Rev. 10/037990

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 21:20:54 ; Search time 1915.63 Seconds
(without alignments)
229.406 Million cell updates/sec

Title: US-10-037-990A-3
Perfect score: 21
Sequence: 1 gtcgtgcagcctccaggaccc 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

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2: gb_htg:*
3: gb_in:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
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27: em_sts:*
28: em_un:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	6	AX147016	AX147016 Sequence
c 2	21	100.0	27	6	BD000273	BD000273 Oligonucl
3	21	100.0	48	6	AX003946	AX003946 Sequence
4	21	100.0	48	6	AX003947	AX003947 Sequence
5	21	100.0	48	6	AX021565	AX021565 Sequence
6	21	100.0	48	6	AX021566	AX021566 Sequence
7	21	100.0	48	6	AX021575	AX021575 Sequence
8	21	100.0	48	6	AX021576	AX021576 Sequence
9	21	100.0	48	6	AX021631	AX021631 Sequence
10	21	100.0	48	6	AX021632	AX021632 Sequence

ALIGNMENTS

RESULT 1
AX147016
LOCUS AX147016 21 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 10 from Patent WO0137291.
ACCESSION AX147016
VERSION AX147016.1 GI:14346287
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 21)
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses thereof
JOURNAL Patent: WO 0137291-A 10 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
source 1. .21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide probe (HCV)"
modified_base 1
/note="Ruthenium3+-(tris-bipyridyl)-derivatisation"
/mod_base=OTHER
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTCGTGCAGCCTCCAGGACCC 21

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BD000273/c
LOCUS BD000273 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD000273
VERSION BD000273.1 GI:18623352
KEYWORDS JP 2000279200-A/11.
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 11 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT OS Artificial Sequence
PN JP 2000279200-A/11
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656

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AX021575
LOCUS       AX021575                  48 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 13 from Patent WO9924606.
ACCESSION   AX021575
VERSION     AX021575.1  GI:10044859
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive nucleic acid detection method
  JOURNAL   Patent: WO 9924606-A 13 20-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
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                     /note="HCV_2B"
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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     10 GTCGTGCAGCCTCCAGGACCC 30


RESULT   8
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LOCUS       AX021576                  48 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 14 from Patent WO9924606.
ACCESSION   AX021576
VERSION     AX021576.1  GI:10044860
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive nucleic acid detection method
  JOURNAL   Patent: WO 9924606-A 14 20-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
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BASE COUNT        9 a     17 c     14 g      8 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 6;  Length 48;
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Db     10 GTCGTGCAGCCTCCAGGACCC 30


RESULT   9
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LOCUS       AX021631                  48 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 10 from Patent WO9923250.
ACCESSION   AX021631
VERSION     AX021631.1  GI:10044914
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923250-A 10 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
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  Query Match             100.0%;  Score 21;  DB 6;  Length 48;
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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          |||||||||||||||||||||
Db     10 GTCGTGCAGCCTCCAGGACCC 30


RESULT  10
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LOCUS       AX021632                  48 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from Patent WO9923250.
ACCESSION   AX021632
VERSION     AX021632.1  GI:10044915
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923250-A 11 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .48
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                     /db_xref="taxon:32630"
                     /note="HCV_MCR"
BASE COUNT        9 a     17 c     14 g      8 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.039;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
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Db 10 GTCGTGCAGCCTCCAGGACCC 30

Search completed: August 26, 2002, 21:20:54
Job time: 7708 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 21:20:54 ; Search time 1915.63 Seconds
(without alignments)
229.406 Million cell updates/sec

Title: US-10-037-990A-3
Perfect score: 21
Sequence: 1 gtcgtgcagcctccaggaccc 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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28: em_un:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	21	100.0	21	6	AX147016	AX147016 Sequence
c 2	21	100.0	27	6	BD000273	BD000273 Oligonucl
3	21	100.0	48	6	AX003946	AX003946 Sequence
4	21	100.0	48	6	AX003947	AX003947 Sequence
5	21	100.0	48	6	AX021565	AX021565 Sequence
6	21	100.0	48	6	AX021566	AX021566 Sequence
7	21	100.0	48	6	AX021575	AX021575 Sequence
8	21	100.0	48	6	AX021576	AX021576 Sequence
9	21	100.0	48	6	AX021631	AX021631 Sequence
10	21	100.0	48	6	AX021632	AX021632 Sequence

ALIGNMENTS

RESULT 1
AX147016
LOCUS AX147016 21 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 10 from Patent WO0137291.
ACCESSION AX147016
VERSION AX147016.1 GI:14346287
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 21)
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses thereof
JOURNAL Patent: WO 0137291-A 10 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide probe (HCV)"
modified_base 1
/note="Ruthenium3+-(tris-bipyridyl)-derivatisation"
/mod_base=OTHER
BASE COUNT 3 a 9 c 6 g 3 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagcctccaggaccc 21
||||||||||||||||||||
Db 1 GTCGTGCAGCCTCCAGGACCC 21

RESULT 2
BD000273/c
LOCUS BD000273 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD000273
VERSION BD000273.1 GI:18623352
KEYWORDS JP 2000279200-A/11.
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 11 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT OS Artificial Sequence
PN JP 2000279200-A/11
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:24:56 ; Search time 450.99 Seconds
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Title: US-10-037-990A-3
Perfect score: 21
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	21	100.0	21	15	AAQ64927	Antisense oligonuc
	2	21	100.0	21	22	AAH25408	Detection probe fo
c	3	21	100.0	22	15	AAQ64928	Antisense oligonuc
c	4	21	100.0	22	15	AAQ64932	Antisense oligonuc
c	5	21	100.0	23	15	AAQ64933	Antisense oligonuc
c	6	21	100.0	23	15	AAQ64937	Antisense oligonuc
c	7	21	100.0	24	15	AAQ64938	Antisense oligonuc
c	8	21	100.0	25	15	AAQ65035	Antisense oligonuc
c	9	21	100.0	26	15	AAQ65030	Antisense oligonuc
c	10	21	100.0	26	15	AAQ65036	Antisense oligonuc
c	11	21	100.0	27	15	AAQ65026	Antisense oligonuc
c	12	21	100.0	27	15	AAQ65031	Antisense oligonuc
c	13	21	100.0	27	15	AAQ65037	Antisense oligonuc
c	14	21	100.0	27	21	AAA74629	HCV probe C96-22-P
c	15	21	100.0	28	15	AAQ65038	Antisense oligonuc
c	16	21	100.0	28	15	AAQ65027	Antisense oligonuc
c	17	21	100.0	28	15	AAQ65032	Antisense oligonuc
c	18	21	100.0	29	15	AAQ65039	Antisense oligonuc
c	19	21	100.0	29	15	AAQ65028	Antisense oligonuc
c	20	21	100.0	29	15	AAQ65033	Antisense oligonuc
c	21	21	100.0	30	15	AAQ65040	Antisense oligonuc
c	22	21	100.0	30	15	AAQ65029	Antisense oligonuc
c	23	21	100.0	30	15	AAQ65034	Antisense oligonuc
	24	21	100.0	48	20	AAZ23541	HCV DNA fragment 1
	25	21	100.0	48	20	AAZ23542	Human DNA fragment

ALIGNMENTS

RESULT 1
AAQ64927/c
ID AAQ64927 standard; DNA; 21 BP.
XX
AC AAQ64927;
XX
DT 19-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 70; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 16-24 bases which is included
CC within the 24 bases from G at position 127 to C at position 150 of
CC AAQ64913 and which contains at least 16 bases from C at position 131
CC to A at position 146. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 21 BP; 3 A; 6 C; 9 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagcctccaggaccc 21
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Db 21 GTCGTGCAGCCTCCAGGACCC 1

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RESULT   2
AAH25408
ID   AAH25408 standard; DNA; 21 BP.
XX
AC   AAH25408;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Detection probe for a HCV DNA fragment.
XX
KW   Magnetic glass particle; nucleic acid purification; probe; ss.
XX
OS   Hepatitis C virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "ruthenium3+-(tris-bipyridyl)-derivatisation"
XX
PN   WO200137291-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11459.
XX
PR   17-NOV-1999;   99EP-0122853.
PR   12-MAY-2000; 2000EP-0110165.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Riedling M,  Geiger A;
XX
DR   WPI; 2001-381247/40.
XX
PT   Novel composition of magnetic glass particles for purification of DNA
PT   or RNA in automated processes  -
XX
PS   Example 7; Page 96; 105pp; English.
XX
CC   The specification describes a composition of magnetic glass particles,
CC   which contain at least one magnetic object with a mean diameter between
CC   5-500 nm. The composition is useful for the purification of nucleic
CC   acids. The composition can be used to process large quantities of
CC   nucleic acid samples, because it does not involve the particles being
CC   centrifuged or the fluids being drawn through glass fiber filters.
CC   The present sequence represents a probe for a HCV DNA fragment. The
CC   DNA fragment can be purified using the method of the invention.
XX
SQ   Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 22;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
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Db      1 gtcgtgcagcctccaggaccc 21


RESULT   3
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ID   AAQ64928 standard; DNA; 22 BP.
XX
AC   AAQ64928;
XX
DT   19-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
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PD   26-FEB-1994.
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PF   23-AUG-1993;   93CA-2104649.
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PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
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PA   (SEKI/) SEKI M.
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PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 70; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 16-24 bases which is included
CC   within the 24 bases from G at position 127 to C at position 150 of
CC   AAQ64913 and which contains at least 16 bases from C at position 131
CC   to A at position 146. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 22 BP; 3 A; 6 C; 10 G; 3 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 15;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
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Db     22 GTCGTGCAGCCTCCAGGACCC 2


RESULT   4
AAQ64932/c
ID   AAQ64932 standard; DNA; 22 BP.
XX
AC   AAQ64932;
XX
DT   19-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
```

```
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 72; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 16-24 bases which is included
CC   within the 24 bases from G at position 127 to C at position 150 of
CC   AAQ64913 and which contains at least 16 bases from C at position 131
CC   to A at position 146. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 22 BP; 4 A; 6 C; 9 G; 3 T; 0 other;


  Query Match           100.0%;  Score 21;  DB 15;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     21 GTCGTGCAGCCTCCAGGACCC 1


RESULT   5
AAQ64933/c
ID   AAQ64933 standard; DNA; 23 BP.
XX
AC   AAQ64933;
XX
DT   19-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 72; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 16-24 bases which is included
CC   within the 24 bases from G at position 127 to C at position 150 of
CC   AAQ64913 and which contains at least 16 bases from C at position 131
CC   to A at position 146. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;


  Query Match           100.0%;  Score 21;  DB 15;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     22 GTCGTGCAGCCTCCAGGACCC 2


RESULT   6
AAQ64937/c
ID   AAQ64937 standard; DNA; 23 BP.
XX
AC   AAQ64937;
XX
DT   19-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 74; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 16-24 bases which is included
CC   within the 24 bases from G at position 127 to C at position 150 of
CC   AAQ64913 and which contains at least 16 bases from C at position 131
CC   to A at position 146. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 23 BP; 4 A; 7 C; 9 G; 3 T; 0 other;


  Query Match           100.0%;  Score 21;  DB 15;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     21 GTCGTGCAGCCTCCAGGACCC 1


RESULT   7
AAQ64938/c
ID   AAQ64938 standard; DNA; 24 BP.
XX
AC   AAQ64938;
XX
DT   19-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
```

```
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 75; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 16-24 bases which is included
CC   within the 24 bases from G at position 127 to C at position 150 of
CC   AAQ64913 and which contains at least 16 bases from C at position 131
CC   to A at position 146. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 10 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     22 GTCGTGCAGCCTCCAGGACCC 2


RESULT   8
AAQ65035/c
ID   AAQ65035 standard; DNA; 25 BP.
XX
AC   AAQ65035;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 117; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 25 BP; 3 A; 6 C; 13 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     25 GTCGTGCAGCCTCCAGGACCC 5


RESULT   9
AAQ65030/c
ID   AAQ65030 standard; DNA; 26 BP.
XX
AC   AAQ65030;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 115; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 26 BP; 4 A; 6 C; 13 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     25 GTCGTGCAGCCTCCAGGACCC 5
```

```
RESULT  10
AAQ65036/c
ID   AAQ65036 standard; DNA; 26 BP.
XX
AC   AAQ65036;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 117; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 26 BP; 4 A; 6 C; 13 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 0.076;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     26 GTCGTGCAGCCTCCAGGACCC 6


RESULT  11
AAQ65026/c
ID   AAQ65026 standard; DNA; 27 BP.
XX
AC   AAQ65026;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 113; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 27 BP; 4 A; 7 C; 13 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     25 GTCGTGCAGCCTCCAGGACCC 5


RESULT  12
AAQ65031/c
ID   AAQ65031 standard; DNA; 27 BP.
XX
AC   AAQ65031;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 115; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
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```
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 27 BP; 5 A; 6 C; 13 G; 3 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 15;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     26 GTCGTGCAGCCTCCAGGACCC 6


RESULT  13
AAQ65037/c
ID   AAQ65037 standard; DNA; 27 BP.
XX
AC   AAQ65037;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 118; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 27 BP; 4 A; 6 C; 14 G; 3 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 15;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     27 GTCGTGCAGCCTCCAGGACCC 7


RESULT  14
AAA74629/c
ID   AAA74629 standard; DNA; 27 BP.
XX
AC   AAA74629;
XX
DT   08-JAN-2001  (first entry)
XX
DE   HCV probe C96-22-PRB.
XX
KW   Hepatitis C virus; HCV; HCV detection; probe; ss.
XX
OS   Hepatitis C virus.
XX
PN   EP1026262-A2.
XX
PD   09-AUG-2000.
XX
PF   01-FEB-2000; 2000EP-0300763.
XX
PR   03-FEB-1999;   99US-0118497.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Linnen JM,  Gorman KM;
XX
DR   WPI; 2000-507254/46.
XX
PT   Detecting hepatitis C virus in biological sample involves amplifying
PT   reverse transcribed products of virus RNA using amplification primers
PT   whose sequences correspond to 5' or 3' non-coding region of the virus
PT   RNA -
XX
PS   Claim 30; Page 27; 28pp; English.
XX
CC   The present sequence is a probe used in a method for detecting hepatitis
CC   C virus (HCV) RNA in biological samples. The HCV RNA is reverse
CC   transcribed to generate cDNA. This is then amplified with primers
CC   corresponding to the 5' or 3' non-coding region of HCV. The product
CC   was captured by hybridisation to oligonucleotide probes, including the
CC   present sequence, which were covalently attached to latex particles and
CC   deposited on the surface of a flow through membrane. The probe/product
CC   complex was reacted with streptavidin-horseradish peroxidase conjugate,
CC   which catalyses the oxidative conversion of a dye precursor to a blue
CC   dye. The method is useful for the diagnosis of HCV infection in
CC   patients, in testing the efficacy of anti-HCV therapeutic regimes, and
CC   in screening blood for HCV-infected samples. The method provides an
CC   improved single-round, reverse transcription/amplification assay which
CC   detects low copy levels of HCV RNA. The primers and assay system are
CC   designed to allow the co-amplification of multiple regions of the HCV
CC   genome, multiple viral species, and an internal positive control (IPC)
CC   RNA (or DNA). Simultaneous amplification/detection of multiple regions
CC   of the HCV genome increases assay sensitivity and the co-amplification
CC   of an IPC decreases the likelihood of false negative results because of
CC   PCR inhibition.
XX
SQ   Sequence 27 BP; 5 A; 8 C; 9 G; 5 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 21;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     21 GTCGTGCAGCCTCCAGGACCC 1


RESULT  15
AAQ65038/c
ID   AAQ65038 standard; DNA; 28 BP.
XX
AC   AAQ65038;
XX
```

DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 118; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AAQ64913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 28 BP; 4 A; 6 C; 15 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagcctccaggaccc 21
||||||||||||||||||||
Db 28 GTCGTGCAGCCTCCAGGACCC 8

RESULT 16
AAQ65027/c
ID AAQ65027 standard; DNA; 28 BP.
XX
AC AAQ65027;
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 113; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AAQ64913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 28 BP; 5 A; 7 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagcctccaggaccc 21
||||||||||||||||||||
Db 26 GTCGTGCAGCCTCCAGGACCC 6

RESULT 17
AAQ65032/c
ID AAQ65032 standard; DNA; 28 BP.
XX
AC AAQ65032;
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 116; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AAQ64913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 28 BP; 5 A; 6 C; 14 G; 3 T; 0 other;

```
  Query Match           100.0%;  Score 21;  DB 15;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     27 GTCGTGCAGCCTCCAGGACCC 7


RESULT  18
AAQ65039/c
ID   AAQ65039 standard; DNA; 29 BP.
XX
AC   AAQ65039;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 119; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 29 BP; 4 A; 6 C; 16 G; 3 T; 0 other;


  Query Match           100.0%;  Score 21;  DB 15;  Length 29;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     29 GTCGTGCAGCCTCCAGGACCC 9


RESULT  19
AAQ65028/c
ID   AAQ65028 standard; DNA; 29 BP.
XX
AC   AAQ65028;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 114; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 29 BP; 5 A; 7 C; 14 G; 3 T; 0 other;


  Query Match           100.0%;  Score 21;  DB 15;  Length 29;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     27 GTCGTGCAGCCTCCAGGACCC 7


RESULT  20
AAQ65033/c
ID   AAQ65033 standard; DNA; 29 BP.
XX
AC   AAQ65033;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
```

```
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 116; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 29 BP; 5 A; 6 C; 15 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 29;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     28 GTCGTGCAGCCTCCAGGACCC 8


RESULT  21
AAQ65040/c
ID   AAQ65040 standard; DNA; 30 BP.
XX
AC   AAQ65040;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 119; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 30 BP; 4 A; 7 C; 16 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     30 GTCGTGCAGCCTCCAGGACCC 10


RESULT  22
AAQ65029/c
ID   AAQ65029 standard; DNA; 30 BP.
XX
AC   AAQ65029;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 114; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 30 BP; 5 A; 7 C; 15 G; 3 T; 0 other;


  Query Match            100.0%;  Score 21;  DB 15;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     28 GTCGTGCAGCCTCCAGGACCC 8


RESULT  23
AAQ65034/c
ID   AAQ65034 standard; DNA; 30 BP.
XX
AC   AAQ65034;
XX
DT   20-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
```

XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 116; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AAQ64913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 30 BP; 5 A; 6 C; 16 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagcctccaggaccc 21
||||||||||||||||||||
Db 29 GTCGTGCAGCCTCCAGGACCC 9

RESULT 24
AAZ23541
ID AAZ23541 standard; DNA; 48 BP.
XX
AC AAZ23541;
XX
DT 21-DEC-1999 (first entry)
XX
DE HCV DNA fragment 1.
XX
KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW cellular; yeast; fungal; primer; ss.
XX
OS Hepatitis C virus.
XX
PN DE19814828-A1.
XX
PD 07-OCT-1999.
XX
PF 02-APR-1998; 98DE-1014828.
XX
PR 02-APR-1998; 98DE-1014828.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Kessler C, Haberhausen G, Batz H, Oerum H;
XX
DR WPI; 1999-552286/47.
XX
PT Nucleic acid amplification assay for detecting viral, bacterial,
PT cellular, yeast or fungal nucleic acids -
XX
PS Disclosure; Fig 4; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises:
CC (a) generating amplification products from a fragment of the nucleic
CC acid, (b) contacting the amplification products with a probe; and
CC (c) detecting hybridization between the amplification product and the
CC probe. The assay is useful for detection of viral, bacterial, cellular,
CC yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
CC or fungal samples, e.g. feces, smears, cell suspensions, cultures or
CC tissue, cell or liquid biopsy samples. This sequence represents a
CC fragment of the HCV genome used in the method of the invention.
XX
SQ Sequence 48 BP; 9 A; 18 C; 14 G; 7 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagcctccaggaccc 21
||||||||||||||||||||
Db 10 gtcgtgcagcctccaggaccc 30

RESULT 25
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ID AAZ23542 standard; DNA; 48 BP.
XX
AC AAZ23542;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human DNA fragment 1.
XX
KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW cellular; yeast; fungal; primer; ss.
XX
OS Homo sapiens.
XX
PN DE19814828-A1.
XX
PD 07-OCT-1999.
XX
PF 02-APR-1998; 98DE-1014828.
XX
PR 02-APR-1998; 98DE-1014828.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Kessler C, Haberhausen G, Batz H, Oerum H;
XX
DR WPI; 1999-552286/47.
XX
PT Nucleic acid amplification assay for detecting viral, bacterial,
PT cellular, yeast or fungal nucleic acids -
XX
PS Disclosure; Fig 4; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises:
CC (a) generating amplification products from a fragment of the nucleic
CC acid, (b) contacting the amplification products with a probe; and
CC (c) detecting hybridization between the amplification product and the
CC probe. The assay is useful for detection of viral, bacterial, cellular,
CC yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
CC or fungal samples, e.g. feces, smears, cell suspensions, cultures or
CC tissue, cell or liquid biopsy samples. This sequence represents a
CC fragment of the human genome which is used in the method of the
CC invention.
XX
SQ Sequence 48 BP; 9 A; 17 C; 14 G; 8 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 gtcgtgcagcctccaggaccc 21
           |||||||||||||||||||||
Db      10 gtcgtgcagcctccaggaccc 30
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Search completed: August 26, 2002, 22:24:56
Job time: 6235 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 20:38:47 ; Search time 119.4 Seconds
(without alignments)
49.374 Million cell updates/sec

Title: US-10-037-990A-1
Perfect score: 24
Sequence: 1 gcagaaagcgtctagccatggcgt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 21

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	24	1	US-08-240-547-5	Sequence 5, Appli
2	24	100.0	24	1	US-08-449-050-17	Sequence 17, Appl
3	24	100.0	24	1	US-08-332-616A-9	Sequence 9, Appli
4	24	100.0	24	1	US-08-317-220-9	Sequence 9, Appli
5	24	100.0	24	1	US-08-675-153-7	Sequence 7, Appli
6	24	100.0	24	2	US-08-738-928-4	Sequence 4, Appli
7	24	100.0	24	2	US-08-841-252-7	Sequence 7, Appli
8	24	100.0	24	2	US-08-881-571-7	Sequence 7, Appli
9	24	100.0	24	4	US-09-282-054-7	Sequence 7, Appli
10	24	100.0	26	1	US-08-240-547-6	Sequence 6, Appli
11	24	100.0	26	2	US-08-738-928-1	Sequence 1, Appli
12	24	100.0	26	3	US-09-039-866-3	Sequence 3, Appli
13	23	95.8	24	3	US-09-078-290A-9	Sequence 9, Appli
14	23	95.8	37	5	PCT-US94-05407-14	Sequence 14, Appl
15	23	95.8	58	5	PCT-US94-05407-12	Sequence 12, Appl
16	21	87.5	21	4	US-09-034-205-25	Sequence 25, Appl
17	21	87.5	21	4	US-08-934-097A-25	Sequence 25, Appl
18	21	87.5	21	4	US-08-851-588-25	Sequence 25, Appl
19	21	87.5	21	4	US-09-677-218B-25	Sequence 25, Appl
20	21	87.5	21	4	US-09-677-192-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-240-547-5
; Sequence 5, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-5

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatggcgt 24
||||||||||||||||||||||||
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 2
US-08-449-050-17
; Sequence 17, Application US/08449050
; Patent No. 5561058
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David
; APPLICANT: Myers, Thomas
; APPLICANT: Sigua, Christopher
; TITLE OF INVENTION: Reagents and Methods for Coupled High
; TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain
; TITLE OF INVENTION: Reactions
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:

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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/449,050
;       FILING DATE:
;       CLASSIFICATION:  435
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
US-08-449-050-17


  Query Match           100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   3
US-08-332-616A-9
; Sequence 9, Application US/08332616A
; Patent No. 5620852
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, LILY
;    APPLICANT:  CIMINO, GEORGE
;    APPLICANT:  ZHU, YU SHENG
;    TITLE OF INVENTION:  NUCLEIC ACID PREPARATION METHODS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,616A
;      FILING DATE:  31-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,545
;      FILING DATE:  19-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  HRI-01202
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-332-616A-9


  Query Match           100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   4
US-08-317-220-9
; Sequence 9, Application US/08317220
; Patent No. 5654179
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, LILY
;    TITLE OF INVENTION:  NUCLEIC ACID PREPARATION METHODS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/317,220
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/044,649
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,545
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/614,921
;      FILING DATE:  14-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  HRI-00542
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-317-220-9


  Query Match           100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   5
US-08-675-153-7
; Sequence 7, Application US/08675153
; Patent No. 5677124
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  DuBois, Dwight
;    APPLICANT:  Winkler, Matthew
;    APPLICANT:  Pasloske, Brittan L.
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT VIRAL
;    TITLE OF INVENTION:  RNA STANDARDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,153
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-675-153-7


  Query Match             100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   6
US-08-738-928-4
; Sequence 4, Application US/08738928
; Patent No. 5837442
;  GENERAL INFORMATION:
;    APPLICANT:  Tsang, Sue Y.
;    TITLE OF INVENTION:  Oligonucleotide Primers for Amplifying
;    TITLE OF INVENTION:  HCV Nucleic Acid
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,928
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  9263
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-738-928-4


  Query Match             100.0%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   7
US-08-841-252-7
; Sequence 7, Application US/08841252
; Patent No. 5919625
;  GENERAL INFORMATION:
;    APPLICANT:  DUBOIS, DWIGHT
;    APPLICANT:  WINKLER, MATTHEW
;    APPLICANT:  PASLOSKE, BRITTAN L.
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT VIRAL RNA
;    TITLE OF INVENTION:  STANDARDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/841,252
;      FILING DATE:  29-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 5,677,124
;      FILING DATE:  03-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILSON, MARK B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:026--1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-300
;      TELEFAX:  512/474-7577
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-841-252-7


  Query Match             100.0%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   8
US-08-881-571-7
; Sequence 7, Application US/08881571
; Patent No. 5939262
;  GENERAL INFORMATION:
;    APPLICANT:  Pasloske, Brittan L.
;    APPLICANT:  DuBois, Dwight
;    APPLICANT:  Brown, David
;    APPLICANT:  Winkler, Matthew
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT RNA PREPARATION
;    TITLE OF INVENTION:  AND UTILIZATION
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/881,571
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/675,153
;      FILING DATE:  03-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,145
;      FILING DATE:  03-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:033
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-3000
;      TELEFAX:  512/474-7577
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-881-571-7


  Query Match            100.0%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   9
US-09-282-054-7
; Sequence 7, Application US/09282054
; Patent No. 6214982
;  GENERAL INFORMATION:
;    APPLICANT:  Pasloske, Brittan L.
;    APPLICANT:  DuBois, Dwight
;    APPLICANT:  Brown, David
;    APPLICANT:  Winkler, Matthew
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT RNA PREPARATION
;    TITLE OF INVENTION:  AND UTILIZATION
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,054
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/881,571
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/675,153
;      FILING DATE:  03-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,145
;      FILING DATE:  03-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:033
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-3000
;      TELEFAX:  512/474-7577
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-282-054-7


  Query Match            100.0%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  10
US-08-240-547-6
; Sequence 6, Application US/08240547
; Patent No. 5527669
;  GENERAL INFORMATION:
;    APPLICANT:  Resnick, Robert M.
;    APPLICANT:  Young, Karen K.Y.
;    TITLE OF INVENTION:  Primers and Probes for Detection of
;    TITLE OF INVENTION:  Hepatitis C and No. 5527669el Variants
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,547
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/918,844
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sias Ph.D., Stacey R.
;      REGISTRATION NUMBER:  32,630
;      REFERENCE/DOCKET NUMBER:  8586
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2863
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-240-547-6


  Query Match             100.0%;  Score 24;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      3 GCAGAAAGCGTCTAGCCATGGCGT 26


RESULT  11
US-08-738-928-1
; Sequence 1, Application US/08738928
; Patent No. 5837442
;  GENERAL INFORMATION:
;    APPLICANT:  Tsang, Sue Y.
;    TITLE OF INVENTION:  Oligonucleotide Primers for Amplifying
;    TITLE OF INVENTION:  HCV Nucleic Acid
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,928
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  9263
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-738-928-1


  Query Match             100.0%;  Score 24;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  12
US-09-039-866-3
; Sequence 3, Application US/09039866
; Patent No. 6001611
;  GENERAL INFORMATION:
;    APPLICANT:  Will, Stephen G.
;    TITLE OF INVENTION:  MODIFIED NUCLEIC ACID AMPLIFICATION
;    TITLE OF INVENTION:  PRIMERS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Roche Molecular Systems
;      STREET:  1080 U.S. Highway 202
;      CITY:  Branchburg
;      STATE:  New Jersey
;      COUNTRY:  United States
;      ZIP:  08876
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/039,866
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  1023P
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-039-866-3


  Query Match             100.0%;  Score 24;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  13
US-09-078-290A-9
; Sequence 9, Application US/09078290A
; Patent No. 6048696
;  GENERAL INFORMATION:
;    APPLICANT:  Hoffman, Leslie M.
;    APPLICANT:  Hawkins, Gregory A.
;    TITLE OF INVENTION:  METHOD FOR IDENTIFYING NUCLEIC ACID MOLECULES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
```

```
;      STREET:  411 East Wisconsin Avenue
;      CITY:  Milwaukee
;      STATE:  Wisconsin
;      COUNTRY:  U.S.A.
;      ZIP:  53202-4497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/078,290A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baker, Jean C.
;      REGISTRATION NUMBER:  35,433
;      REFERENCE/DOCKET NUMBER:  310307.90100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (414) 277-5709
;      TELEFAX:  (414) 271-3552
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Oligonucleotide
US-09-078-290A-9


  Query Match             95.8%;  Score 23;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 cagaaagcgtctagccatggcgt 24
          |||||||||||||||||||||||
Db      1 CAGAAAGCGTCTAGCCATGGCGT 23


RESULT  14
PCT-US94-05407-14
; Sequence 14, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-14


  Query Match             95.8%;  Score 23;  DB 5;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 cagaaagcgtctagccatggcgt 24
          |||||||||||||||||||||||
Db     14 CAGAAAGCGTCTAGCCATGGCGT 36


RESULT  15
PCT-US94-05407-12
; Sequence 12, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  58 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-12


  Query Match             95.8%;  Score 23;  DB 5;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 cagaaagcgtctagccatggcgt 24
          |||||||||||||||||||||||
Db     11 CAGAAAGCGTCTAGCCATGGCGT 33


RESULT  16
US-09-034-205-25
; Sequence 25, Application US/09034205
; Patent No. 6194149
;  GENERAL INFORMATION:
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    APPLICANT:  Fors, Lance
;    APPLICANT:  Neri, Bruce P.
;    TITLE OF INVENTION:  TARGET-DEPENDENT REACTIONS USING
;    TITLE OF INVENTION:  STRUCTURE-BRIDGING OLIGONUCLEOTIDES
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/034,205
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MacKnight, Kamrin T.
;       REGISTRATION NUMBER:  38,230
;       REFERENCE/DOCKET NUMBER:  FORS-03268
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  25:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "DNA"
US-09-034-205-25


  Query Match             87.5%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21


RESULT  17
US-08-934-097A-25
; Sequence 25, Application US/08934097A
; Patent No. 6210880
;  GENERAL INFORMATION:
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Brow, Mary Ann D.
;    APPLICANT:  Fors, Lance
;    APPLICANT:  Neri, Bruce P.
;    TITLE OF INVENTION:  Polymorphism Analysis By Nucleic Acid
;    TITLE OF INVENTION:  Structure Probing With Structure-Bridging
;    TITLE OF INVENTION:  Oligonucleotides.
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/934,097A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  FORS-02980
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "DNA"
US-08-934-097A-25


  Query Match             87.5%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
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          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21


RESULT  18
US-08-851-588-25
; Sequence 25, Application US/08851588
; Patent No. 6214545
;  GENERAL INFORMATION:
;    APPLICANT:  Dong, Fang
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Prudent, James R.
;    APPLICANT:  Dahlberg, James E.
;    APPLICANT:  Fors, Lance
;    TITLE OF INVENTION:  Polymorphism Analysis By Nucleic Acid
;    TITLE OF INVENTION:  Structure Probing
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/851,588
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02777
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "DNA"
US-08-851-588-25


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  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21
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RESULT  19
US-09-677-218B-25
; Sequence 25, Application US/09677218B
; Patent No. 6355437
;  GENERAL INFORMATION:
;       APPLICANT: Lyamichev, Victor I.
;                  Brow, Mary Ann D.
;                  Fors, Lance
;                  Neri, Bruce P.
;       TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
;                           STRUCTURE-BRIDGING OLIGONUCLEOTIDES
;       NUMBER OF SEQUENCES: 68
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MEDLEN & CARROLL, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/677,218B
;            FILING DATE: 02-Oct-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/034,205
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: MacKnight, Kamrin T.
;            REGISTRATION NUMBER: 38,230
;            REFERENCE/DOCKET NUMBER: FORS-03268
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 21 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-677-218B-25


  Query Match             87.5%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21


RESULT  20
US-09-677-192-25
; Sequence 25, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
;  APPLICANT:  Lyamichev, Victor I.
;  APPLICANT:  Brow, Mary Ann D.
;  APPLICANT:  Fors, Lance
;  APPLICANT:  Neri, Bruce P.
;  TITLE OF INVENTION:  TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES
;  FILE REFERENCE:  FORS-04708
;  CURRENT APPLICATION NUMBER: US/09/677,192
;  CURRENT FILING DATE:  2000-10-02
;  PRIOR APPLICATION NUMBER:  09/034,205
;  PRIOR FILING DATE:  1998-03-03
;  NUMBER OF SEQ ID NOS:  68
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-677-192-25


  Query Match             87.5%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 gcagaaagcgtctagccatgg 21


Search completed: August 26, 2002, 22:17:11
Job time: 5904 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:17:11 ; Search time 119.4 Seconds
(without alignments)
49.374 Million cell updates/sec

Title: US-10-037-990A-2
Perfect score: 24
Sequence: 1 ctcgcaagcaccctatcaggcagt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 21

Total number of hits satisfying chosen parameters: 41

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	1	US-08-240-547-18	Sequence 18, Appl
	2	24	100.0	24	1	US-08-449-050-16	Sequence 16, Appl
	3	24	100.0	24	1	US-08-332-616A-8	Sequence 8, Appli
	4	24	100.0	24	1	US-08-317-220-8	Sequence 8, Appli
	5	24	100.0	24	1	US-08-675-153-8	Sequence 8, Appli
c	6	24	100.0	24	1	US-08-244-116B-51	Sequence 51, Appl
	7	24	100.0	24	2	US-08-738-928-5	Sequence 5, Appli
	8	24	100.0	24	2	US-08-841-252-8	Sequence 8, Appli
	9	24	100.0	24	2	US-08-881-571-8	Sequence 8, Appli
	10	24	100.0	24	4	US-09-282-054-8	Sequence 8, Appli
	11	24	100.0	26	1	US-08-240-547-19	Sequence 19, Appl
	12	24	100.0	26	2	US-08-256-568B-4	Sequence 4, Appli
	13	24	100.0	26	4	US-09-038-369B-4	Sequence 4, Appli
	14	24	100.0	27	5	PCT-US93-00928-1	Sequence 1, Appli
	15	24	100.0	28	3	US-08-474-700B-12	Sequence 12, Appl
	16	24	100.0	28	5	PCT-US95-05812-12	Sequence 12, Appl
	17	24	100.0	33	1	US-08-438-639-51	Sequence 51, Appl
	18	24	100.0	33	1	US-07-813-338A-51	Sequence 51, Appl
	19	24	100.0	33	2	US-08-470-124-61	Sequence 61, Appl
	20	24	100.0	33	3	US-08-441-971-127	Sequence 127, App
	21	24	100.0	33	4	US-08-221-653-127	Sequence 127, App
	22	24	100.0	33	4	US-08-442-144A-127	Sequence 127, App
	23	24	100.0	33	4	US-08-441-970-127	Sequence 127, App
	24	24	100.0	53	1	US-08-429-181-16	Sequence 16, Appl
	25	24	100.0	53	1	US-08-429-181-49	Sequence 49, Appl
	26	24	100.0	53	1	US-08-164-388-16	Sequence 16, Appl
	27	24	100.0	53	1	US-08-164-388-49	Sequence 49, Appl
c	28	24	100.0	57	1	US-08-356-287-36	Sequence 36, Appl
c	29	24	100.0	57	5	PCT-US93-04863-36	Sequence 36, Appl
	30	24	100.0	64	1	US-08-429-181-31	Sequence 31, Appl
	31	24	100.0	64	1	US-08-164-388-31	Sequence 31, Appl
	32	23	95.8	23	1	US-08-356-287-25	Sequence 25, Appl
	33	23	95.8	23	5	PCT-US93-04863-25	Sequence 25, Appl
	34	23	95.8	29	1	US-08-240-547-20	Sequence 20, Appl
c	35	22	91.7	22	1	US-08-356-287-27	Sequence 27, Appl
c	36	22	91.7	22	5	PCT-US93-04863-27	Sequence 27, Appl
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	39	21	87.5	28	3	US-09-039-866-4	Sequence 4, Appli
c	40	21	87.5	28	3	US-08-474-700B-35	Sequence 35, Appl
c	41	21	87.5	28	5	PCT-US95-05812-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-240-547-18
; Sequence 18, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-18

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ctcgcaagcaccctatcaggcagt 24
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Db      1 CTCGCAAGCACCCTATCAGGCAGT 24
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RESULT   2
US-08-449-050-16
; Sequence 16, Application US/08449050
; Patent No. 5561058
;  GENERAL INFORMATION:
;    APPLICANT:  Gelfand, David
;    APPLICANT:  Myers, Thomas
;    APPLICANT:  Sigua, Christopher
;    TITLE OF INVENTION:  Reagents and Methods for Coupled High
;    TITLE OF INVENTION:  Temperature Reverse Transcription and Polymerase Chain
;    TITLE OF INVENTION:  Reactions
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/449,050
;      FILING DATE:
;      CLASSIFICATION:  435
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
US-08-449-050-16


  Query Match             100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   3
US-08-332-616A-8
; Sequence 8, Application US/08332616A
; Patent No. 5620852
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, LILY
;    APPLICANT:  CIMINO, GEORGE
;    APPLICANT:  ZHU, YU SHENG
;    TITLE OF INVENTION:  NUCLEIC ACID PREPARATION METHODS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,616A
;      FILING DATE:  31-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,545
;      FILING DATE:  19-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  HRI-01202
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-332-616A-8


  Query Match             100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   4
US-08-317-220-8
; Sequence 8, Application US/08317220
; Patent No. 5654179
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, LILY
;    TITLE OF INVENTION:  NUCLEIC ACID PREPARATION METHODS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/317,220
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/044,649
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,545
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/614,921
;      FILING DATE:  14-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  HRI-00542
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-317-220-8


  Query Match             100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   5
US-08-675-153-8
; Sequence 8, Application US/08675153
; Patent No. 5677124
;  GENERAL INFORMATION:
;    APPLICANT:  DuBois, Dwight
;    APPLICANT:  Winkler, Matthew
;    APPLICANT:  Pasloske, Brittan L.
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT VIRAL
;    TITLE OF INVENTION:  RNA STANDARDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/675,153
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-675-153-8


  Query Match             100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   6
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; Sequence 51, Application US/08244116B
; Patent No. 5763159
;  GENERAL INFORMATION:
;    APPLICANT:  Simmonds, Peter
;    APPLICANT:  Chan, Shiu-Wan
;    APPLICANT:  Yap, Peng L.
;    TITLE OF INVENTION:  Hepatitis-C Virus Testing
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 5763159th Carolina
;      COUNTRY:  United States
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0. Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,116B
;      FILING DATE:  15-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02143
;      FILING DATE:  20-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  1749-125
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  704-377-1561
;      TELEFAX:  704-334-2014
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "synthetic DNA
;      DESCRIPTION:  oligonucleotide"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Hepatitis-C virus
US-08-244-116B-51


  Query Match             100.0%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     24 CTCGCAAGCACCCTATCAGGCAGT 1


RESULT   7
US-08-738-928-5
; Sequence 5, Application US/08738928
; Patent No. 5837442
;  GENERAL INFORMATION:
;    APPLICANT:  Tsang, Sue Y.
;    TITLE OF INVENTION:  Oligonucleotide Primers for Amplifying
;    TITLE OF INVENTION:  HCV Nucleic Acid
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/738,928
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petry, Douglas A.
;       REGISTRATION NUMBER:  35,321
;       REFERENCE/DOCKET NUMBER:  9263
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 814-2974
;       TELEFAX:  (510) 814-2977
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-738-928-5


  Query Match             100.0%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   8
US-08-841-252-8
; Sequence 8, Application US/08841252
; Patent No. 5919625
;  GENERAL INFORMATION:
;    APPLICANT:  DUBOIS, DWIGHT
;    APPLICANT:  WINKLER, MATTHEW
;    APPLICANT:  PASLOSKE, BRITTAN L.
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT VIRAL RNA
;    TITLE OF INVENTION:  STANDARDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/841,252
;      FILING DATE:  29-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 5,677,124
;      FILING DATE:  03-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILSON, MARK B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:026--1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-300
;      TELEFAX:  512/474-7577
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-841-252-8


  Query Match             100.0%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   9
US-08-881-571-8
; Sequence 8, Application US/08881571
; Patent No. 5939262
;  GENERAL INFORMATION:
;    APPLICANT:  Pasloske, Brittan L.
;    APPLICANT:  DuBois, Dwight
;    APPLICANT:  Brown, David
;    APPLICANT:  Winkler, Matthew
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT RNA PREPARATION
;    TITLE OF INVENTION:  AND UTILIZATION
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/881,571
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/675,153
;      FILING DATE:  03-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,145
;      FILING DATE:  03-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:033
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-3000
;      TELEFAX:  512/474-7577
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-881-571-8


  Query Match             100.0%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24
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RESULT  10
US-09-282-054-8
; Sequence 8, Application US/09282054
; Patent No. 6214982
;  GENERAL INFORMATION:
;    APPLICANT:  Pasloske, Brittan L.
;    APPLICANT:  DuBois, Dwight
;    APPLICANT:  Brown, David
;    APPLICANT:  Winkler, Matthew
;    TITLE OF INVENTION:  RIBONUCLEASE RESISTANT RNA PREPARATION
;    TITLE OF INVENTION:  AND UTILIZATION
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,054
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/881,571
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/675,153
;      FILING DATE:  03-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,145
;      FILING DATE:  03-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  AMBI:033
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-3000
;      TELEFAX:  512/474-7577
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-282-054-8


  Query Match           100.0%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT  11
US-08-240-547-19
; Sequence 19, Application US/08240547
; Patent No. 5527669
;  GENERAL INFORMATION:
;    APPLICANT:  Resnick, Robert M.
;    APPLICANT:  Young, Karen K.Y.
;    TITLE OF INVENTION:  Primers and Probes for Detection of
;    TITLE OF INVENTION:  Hepatitis C and No. 5527669el Variants
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,547
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/918,844
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sias Ph.D., Stacey R.
;      REGISTRATION NUMBER:  32,630
;      REFERENCE/DOCKET NUMBER:  8586
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2863
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-240-547-19


  Query Match           100.0%;  Score 24;  DB 1;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  12
US-08-256-568B-4
; Sequence 4, Application US/08256568B
; Patent No. 5846704
;  GENERAL INFORMATION:
;    APPLICANT:  MAERTENS, GEERT; STUYVER, LIEVEN;
;    APPLICANT:  ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
;    TITLE OF INVENTION:  PROCESS FOR TYPING OF HCV
;    TITLE OF INVENTION:  ISOLATES
;    NUMBER OF SEQUENCES:  97
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/256,568B
;      FILING DATE:  18-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03325
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;      FILING DATE:  26-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/93/402,129.6
;      FILING DATE:  31-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403,222.0
;      FILING DATE:  27-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  HCV
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  HCV
;      MAP POSITION:  Position -29 of 5' end
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..26
;      OTHER INFORMATION:  /standard_name=
;      OTHER INFORMATION:  "Universal HCV primer HcPr96"
US-08-256-568B-4


  Query Match             100.0%;  Score 24;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  13
US-09-038-369B-4
; Sequence 4, Application US/09038369B
; Patent No. 6171784
;  GENERAL INFORMATION:
;    APPLICANT:  MAERTENS, GEERT; STUYVER, LIEVEN;
;    APPLICANT:  ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
;    TITLE OF INVENTION:  PROCESS FOR TYPING OF HCV
;    TITLE OF INVENTION:  ISOLATES
;    NUMBER OF SEQUENCES:  97
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,369B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/256,568
;      FILING DATE:  18-JUL-1994
;      APPLICATION NUMBER:  PCT/EP93/03325
;      FILING DATE:  26-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/93/402,129.6
;      FILING DATE:  31-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403,222.0
;      FILING DATE:  27-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  HCV
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  HCV
;      MAP POSITION:  Position -29 of 5' end
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..26
;      OTHER INFORMATION:  /standard_name=
;      OTHER INFORMATION:  "Universal HCV primer HcPr96"
US-09-038-369B-4


  Query Match             100.0%;  Score 24;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  14
PCT-US93-00928-1
; Sequence 1, Application PC/TUS9300928
;  GENERAL INFORMATION:
;    APPLICANT:  TASSOPOULOS, NIC C.
;    APPLICANT:  HATZAKIS, ANGELOS E.
;    APPLICANT:  KUHNS, MARY C.
;    APPLICANT:  TROONEN, HUGO
;    TITLE OF INVENTION:  NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND ME
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ABBOTT LABORATORIES  D377/AP6D
;      STREET:  ONE ABBOTT PARK ROAD
;      CITY:  ABBOTT PARK
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00928
;      FILING DATE:  19930203
;      CLASSIFICATION:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  POREMBSKI, PRISCILLA E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5132.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-6365
;      TELEFAX:  708-937-9556
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US93-00928-1


  Query Match           100.0%;  Score 24;  DB 5;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  15
US-08-474-700B-12
; Sequence 12, Application US/08474700B
; Patent No. 6001990
;  GENERAL INFORMATION:
;    APPLICANT:  Wands, Jack
;    APPLICANT:  Wakita, Takaji
;    APPLICANT:  Moradpour, Darius
;    TITLE OF INVENTION:  ANTISENSE INHIBITION OF HEPATITIS C
;    TITLE OF INVENTION:  VIRUS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,700B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,382
;      FILING DATE:  10 May 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/279001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-474-700B-12


  Query Match           100.0%;  Score 24;  DB 3;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      2 CTCGCAAGCACCCTATCAGGCAGT 25


RESULT  16
PCT-US95-05812-12
; Sequence 12, Application PC/TUS9505812
;  GENERAL INFORMATION:
;    APPLICANT:  Wakita, Takaji
;    APPLICANT:  Wands, Jack
;    TITLE OF INVENTION:  ANTISENSE INHIBITION OF
;    TITLE OF INVENTION:  HEPATITIS C VIRUS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05812
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,382
;      FILING DATE:  10 May 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/221001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-05812-12


  Query Match           100.0%;  Score 24;  DB 5;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      2 CTCGCAAGCACCCTATCAGGCAGT 25


RESULT  17
US-08-438-639-51
; Sequence 51, Application US/08438639
; Patent No. 5712383
;  GENERAL INFORMATION:
;    APPLICANT:  Sheridan, Patrick
;    APPLICANT:  Chang, Chu-An
;    APPLICANT:  Running, Joyce
;    APPLICANT:  Urdea, Michael S.
;    TITLE OF INVENTION:  PROCESS FOR IMMOBILIZING NUCLEIC ACID
;    TITLE OF INVENTION:  PROBES ON POLYSTYRENE SURFACES
```

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;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - R440
;      STREET:  P.O. Box 8097
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94662-8097
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,639
;      FILING DATE:  10-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/813,338
;      FILING DATE:  23-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Kenneth, M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0232.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-438-639-51


  Query Match             100.0%;  Score 24;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  18
US-07-813-338A-51
; Sequence 51, Application US/07813338A
; Patent No. 5747244
;  GENERAL INFORMATION:
;    APPLICANT:  Sheridan, Patrick
;    APPLICANT:  Chang, Chu-An
;    APPLICANT:  Running, Joyce
;    APPLICANT:  Urdea, Michael S.
;    TITLE OF INVENTION:  PROCESS FOR IMMOBILIZING NUCLEIC ACID
;    TITLE OF INVENTION:  PROBES ON POLYSTYRENE SURFACES
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - R440
;      STREET:  P.O. Box 8097
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94662-8097
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/813,338A
;      FILING DATE:  23-DEC-1991
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Kenneth, M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0232.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-813-338A-51


  Query Match             100.0%;  Score 24;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  19
US-08-470-124-61
; Sequence 61, Application US/08470124
; Patent No. 5849481
;  GENERAL INFORMATION:
;    APPLICANT:  Urdea, Michael S.
;    APPLICANT:  Horn, Thomas
;    APPLICANT:  Chang, Chu-An
;    APPLICANT:  Warner, Brian
;    APPLICANT:  Fultz, Timothy J.
;    TITLE OF INVENTION:  LARGE COMB-TYPE BRANCHED
;    TITLE OF INVENTION:  POLYNUCLEOTIDES
;    NUMBER OF SEQUENCES:  87
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,124
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/813,588
;      FILING DATE:  23 December 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ciotti, Thomas E.
;      REGISTRATION NUMBER:  21,013
;      REFERENCE/DOCKET NUMBER:  22300-20104.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-327-2951
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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```
US-08-470-124-61


  Query Match             100.0%;  Score 24;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  20
US-08-441-971-127
; Sequence 127, Application US/08441971
; Patent No. 6071693
;  GENERAL INFORMATION:
;    APPLICANT:  Tai-An Cha
;    TITLE OF INVENTION:  HCV GENOMIC SEQUENCES FOR
;    TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS Version 3.3
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,971
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,653
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/881,528
;      FILING DATE:
;      APPLICATION NUMBER:  07/697,326
;      FILING DATE:  8 May 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janiuk, Anthony J.
;      REGISTRATION NUMBER:  29,809
;      REFERENCE/DOCKET NUMBER:  C0772/7000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 720-3500
;      TELEFAX:  (617) 720-2441
;      TELEX:  EZEKIEL
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-441-971-127


  Query Match             100.0%;  Score 24;  DB 3;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  21
US-08-221-653-127
; Sequence 127, Application US/08221653
; Patent No. 6190864
;  GENERAL INFORMATION:
;    APPLICANT:  Tai-An Cha
;    TITLE OF INVENTION:  HCV GENOMIC SEQUENCES FOR
;    TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS Version 3.3
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/881,528
;      FILING DATE:
;      APPLICATION NUMBER:  07/697,326
;      FILING DATE:  8 May 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janiuk, Anthony J.
;      REGISTRATION NUMBER:  29,809
;      REFERENCE/DOCKET NUMBER:  C0772/7000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 720-3500
;      TELEFAX:  (617) 720-2441
;      TELEX:  EZEKIEL
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-221-653-127


  Query Match             100.0%;  Score 24;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  22
US-08-442-144A-127
; Sequence 127, Application US/08442144A
; Patent No. 6214583
;  GENERAL INFORMATION:
;    APPLICANT:  Tai-An Cha
;    APPLICANT:  Eileen Beall
;    APPLICANT:  Bruce Irvine
;    APPLICANT:  Janice Kolberg
;    APPLICANT:  Michael S. Urdea
;    TITLE OF INVENTION:  HCV GENOMIC SEQUENCES FOR
;    TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;    NUMBER OF SEQUENCES:  148
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  California
```

```
;       COUNTRY:  USA
;       ZIP:  94608-2916
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 Inch
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows NT
;       SOFTWARE:  Microsoft Word 97
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/442,144A
;       FILING DATE:  MAY 16, 1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/221,653
;       FILING DATE:  APRIL 1, 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Doreen Yatko Trujillo
;       REGISTRATION NUMBER:  35,719
;       REFERENCE/DOCKET NUMBER:  CHIR-0121
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-568-3100
;       TELEFAX:  215-568-3439
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  127:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  33 Nucleotides
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
;     MOLECULE TYPE:  DNA
US-08-442-144A-127


  Query Match             100.0%;  Score 24;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db       7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  23
US-08-441-970-127
; Sequence 127, Application US/08441970
; Patent No. 6297370
;  GENERAL INFORMATION:
;    APPLICANT:  Tai-An Cha
;    TITLE OF INVENTION:  HCV GENOMIC SEQUENCES FOR
;    TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS Version 3.3
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,970
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/881,528
;      FILING DATE:  08-MAY-1992
;      APPLICATION NUMBER:  07/697,326
;      FILING DATE:  8 May 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janiuk, Anthony J.
;      REGISTRATION NUMBER:  29,809
;      REFERENCE/DOCKET NUMBER:  C0772/7000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 720-3500
;      TELEFAX:  (617) 720-2441
;      TELEX:  EZEKIEL
;  INFORMATION FOR SEQ ID NO:  127:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-441-970-127


  Query Match             100.0%;  Score 24;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db       7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  24
US-08-429-181-16
; Sequence 16, Application US/08429181
; Patent No. 5635352
;  GENERAL INFORMATION:
;    APPLICANT:  URDEA, MICHAEL S.
;    APPLICANT:  FULTZ, TIMOTHY
;    APPLICANT:  WARNER, BRIAN D.
;    APPLICANT:  COLLINS, MARK
;    TITLE OF INVENTION:  SOLUTION PHASE NUCLEIC ACID SANDWICH
;    TITLE OF INVENTION:  ASSAYS HAVING REDUCED BACKGROUND NOISE
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - INTELLECTUAL PROPERTY
;      ADDRESSEE:  R440
;      STREET:  4560 HORTON STREET
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/429,181
;      FILING DATE:  26-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/164,388
;      FILING DATE:  08-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDMAN, KENNETH M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0300.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-429-181-16
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```
  Query Match           100.0%;  Score 24;  DB 1;  Length 53;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  25
US-08-429-181-49
; Sequence 49, Application US/08429181
; Patent No. 5635352
;  GENERAL INFORMATION:
;    APPLICANT:  URDEA, MICHAEL S.
;    APPLICANT:  FULTZ, TIMOTHY
;    APPLICANT:  WARNER, BRIAN D.
;    APPLICANT:  COLLINS, MARK
;    TITLE OF INVENTION:  SOLUTION PHASE NUCLEIC ACID SANDWICH
;    TITLE OF INVENTION:  ASSAYS HAVING REDUCED BACKGROUND NOISE
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - INTELLECTUAL PROPERTY
;      ADDRESSEE:  R440
;      STREET:  4560 HORTON STREET
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/429,181
;      FILING DATE:  26-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/164,388
;      FILING DATE:  08-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDMAN, KENNETH M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0300.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-429-181-49


  Query Match           100.0%;  Score 24;  DB 1;  Length 53;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  26
US-08-164-388-16
; Sequence 16, Application US/08164388
; Patent No. 5681697
;  GENERAL INFORMATION:
;    APPLICANT:  URDEA, MICHAEL S.
;    APPLICANT:  FULTZ, TIMOTHY
;    APPLICANT:  WARNER, BRIAN D.
;    APPLICANT:  COLLINS, MARK
;    TITLE OF INVENTION:  SOLUTION PHASE NUCLEIC ACID SANDWICH
;    TITLE OF INVENTION:  ASSAYS HAVING REDUCED BACKGROUND NOISE
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - INTELLECTUAL PROPERTY
;      ADDRESSEE:  R440
;      STREET:  4560 HORTON STREET
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/164,388
;      FILING DATE:  08-DEC-1993
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDMAN, KENNETH M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0300.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-164-388-16


  Query Match           100.0%;  Score 24;  DB 1;  Length 53;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  27
US-08-164-388-49
; Sequence 49, Application US/08164388
; Patent No. 5681697
;  GENERAL INFORMATION:
;    APPLICANT:  URDEA, MICHAEL S.
;    APPLICANT:  FULTZ, TIMOTHY
;    APPLICANT:  WARNER, BRIAN D.
;    APPLICANT:  COLLINS, MARK
;    TITLE OF INVENTION:  SOLUTION PHASE NUCLEIC ACID SANDWICH
;    TITLE OF INVENTION:  ASSAYS HAVING REDUCED BACKGROUND NOISE
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - INTELLECTUAL PROPERTY
;      ADDRESSEE:  R440
;      STREET:  4560 HORTON STREET
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94608-2916
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/164,388
;      FILING DATE:  08-DEC-1993
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDMAN, KENNETH M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0300.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-164-388-49


  Query Match             100.0%;  Score 24;  DB 1;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  28
US-08-356-287-36/c
; Sequence 36, Application US/08356287
; Patent No. 5686272
;  GENERAL INFORMATION:
;    APPLICANT:  Ronald L. Marshall
;    APPLICANT:  John J. Carrino
;    APPLICANT:  Joann Sustachek
;    TITLE OF INVENTION:  AMPLIFICATION OF RNA SEQUENCES USING
;    TITLE OF INVENTION:  THE LIGASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy diskette
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.0.1
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,287
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/891,543
;      FILING DATE:  29 MAY 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul D. Yasger
;      REGISTRATION NUMBER:  37,477
;      REFERENCE/DOCKET NUMBER:  5172.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-2341
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  57
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
US-08-356-287-36


  Query Match             100.0%;  Score 24;  DB 1;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     57 CTCGCAAGCACCCTATCAGGCAGT 34


RESULT  29
PCT-US93-04863-36/c
; Sequence 36, Application PC/TUS9304863
;  GENERAL INFORMATION:
;    APPLICANT:  Ronald L. Marshall
;    APPLICANT:  John J. Carrino
;    APPLICANT:  Joann C. Sustachek
;    APPLICANT:  ABBOTT LABORATORIES
;    TITLE OF INVENTION:  AMPLIFICATION OF RNA SEQUENCES
;    TITLE OF INVENTION:  USING THE LIGASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  One Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/04863
;      FILING DATE:  19930524
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/891,543
;      FILING DATE:  29 MAY 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Thomas D. Brainard
;      REGISTRATION NUMBER:  32,459
;      REFERENCE/DOCKET NUMBER:  5172.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-4884
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  57
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
PCT-US93-04863-36


  Query Match             100.0%;  Score 24;  DB 5;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     57 CTCGCAAGCACCCTATCAGGCAGT 34
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RESULT  30
US-08-429-181-31
; Sequence 31, Application US/08429181
; Patent No. 5635352
;  GENERAL INFORMATION:
;    APPLICANT:  URDEA, MICHAEL S.
;    APPLICANT:  FULTZ, TIMOTHY
;    APPLICANT:  WARNER, BRIAN D.
;    APPLICANT:  COLLINS, MARK
;    TITLE OF INVENTION:  SOLUTION PHASE NUCLEIC ACID SANDWICH
;    TITLE OF INVENTION:  ASSAYS HAVING REDUCED BACKGROUND NOISE
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - INTELLECTUAL PROPERTY
;      ADDRESSEE:  R440
;      STREET:  4560 HORTON STREET
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/429,181
;      FILING DATE:  26-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/164,388
;      FILING DATE:  08-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDMAN, KENNETH M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0300.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  64 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-429-181-31


  Query Match             100.0%;  Score 24;  DB 1;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db      23 CTCGCAAGCACCCTATCAGGCAGT 46


RESULT  31
US-08-164-388-31
; Sequence 31, Application US/08164388
; Patent No. 5681697
;  GENERAL INFORMATION:
;    APPLICANT:  URDEA, MICHAEL S.
;    APPLICANT:  FULTZ, TIMOTHY
;    APPLICANT:  WARNER, BRIAN D.
;    APPLICANT:  COLLINS, MARK
;    TITLE OF INVENTION:  SOLUTION PHASE NUCLEIC ACID SANDWICH
;    TITLE OF INVENTION:  ASSAYS HAVING REDUCED BACKGROUND NOISE
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - INTELLECTUAL PROPERTY
;      ADDRESSEE:  R440
;      STREET:  4560 HORTON STREET
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/164,388
;      FILING DATE:  08-DEC-1993
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDMAN, KENNETH M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0300.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  64 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-164-388-31


  Query Match             100.0%;  Score 24;  DB 1;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db      23 CTCGCAAGCACCCTATCAGGCAGT 46


RESULT  32
US-08-356-287-25
; Sequence 25, Application US/08356287
; Patent No. 5686272
;  GENERAL INFORMATION:
;    APPLICANT:  Ronald L. Marshall
;    APPLICANT:  John J. Carrino
;    APPLICANT:  Joann Sustachek
;    TITLE OF INVENTION:  AMPLIFICATION OF RNA SEQUENCES USING
;    TITLE OF INVENTION:  THE LIGASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy diskette
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.0.1
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,287
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/891,543
```

```
;      FILING DATE:  29 MAY 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul D. Yasger
;      REGISTRATION NUMBER:  37,477
;      REFERENCE/DOCKET NUMBER:  5172.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-2341
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid (synthetic DNA)
US-08-356-287-25


  Query Match             95.8%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          |||||||||||||||||||||||
Db      1 TCGCAAGCACCCTATCAGGCAGT 23


RESULT  33
PCT-US93-04863-25
; Sequence 25, Application PC/TUS9304863
;  GENERAL INFORMATION:
;    APPLICANT:  Ronald L. Marshall
;    APPLICANT:  John J. Carrino
;    APPLICANT:  Joann C. Sustachek
;    APPLICANT:  ABBOTT LABORATORIES
;    TITLE OF INVENTION:  AMPLIFICATION OF RNA SEQUENCES
;    TITLE OF INVENTION:  USING THE LIGASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  One Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/04863
;      FILING DATE:  19930524
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/891,543
;      FILING DATE:  29 MAY 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Thomas D. Brainard
;      REGISTRATION NUMBER:  32,459
;      REFERENCE/DOCKET NUMBER:  5172.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-4884
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid (synthetic DNA)
PCT-US93-04863-25


  Query Match             95.8%;  Score 23;  DB 5;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          |||||||||||||||||||||||
Db      1 TCGCAAGCACCCTATCAGGCAGT 23


RESULT  34
US-08-240-547-20
; Sequence 20, Application US/08240547
; Patent No. 5527669
;  GENERAL INFORMATION:
;    APPLICANT:  Resnick, Robert M.
;    APPLICANT:  Young, Karen K.Y.
;    TITLE OF INVENTION:  Primers and Probes for Detection of
;    TITLE OF INVENTION:  Hepatitis C and No. 5527669el Variants
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,547
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/918,844
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sias Ph.D., Stacey R.
;      REGISTRATION NUMBER:  32,630
;      REFERENCE/DOCKET NUMBER:  8586
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2863
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-240-547-20


  Query Match             95.8%;  Score 23;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          |||||||||||||||||||||||
Db      7 TCGCAAGCACCCTATCAGGCAGT 29


RESULT  35
US-08-356-287-27/c
; Sequence 27, Application US/08356287
; Patent No. 5686272
;  GENERAL INFORMATION:
;    APPLICANT:  Ronald L. Marshall
;    APPLICANT:  John J. Carrino
;    APPLICANT:  Joann Sustachek
```

```
;    TITLE OF INVENTION:  AMPLIFICATION OF RNA SEQUENCES USING
;    TITLE OF INVENTION:  THE LIGASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy diskette
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.0.1
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,287
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/891,543
;      FILING DATE:  29 MAY 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul D. Yasger
;      REGISTRATION NUMBER:  37,477
;      REFERENCE/DOCKET NUMBER:  5172.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-2341
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid (synthetic DNA)
US-08-356-287-27


  Query Match             91.7%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggca 22
          ||||||||||||||||||||||
Db     22 CTCGCAAGCACCCTATCAGGCA 1


RESULT  36
PCT-US93-04863-27/c
; Sequence 27, Application PC/TUS9304863
;  GENERAL INFORMATION:
;    APPLICANT:  Ronald L. Marshall
;    APPLICANT:  John J. Carrino
;    APPLICANT:  Joann C. Sustachek
;    APPLICANT:  ABBOTT LABORATORIES
;    TITLE OF INVENTION:  AMPLIFICATION OF RNA SEQUENCES
;    TITLE OF INVENTION:  USING THE LIGASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  One Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/04863
;      FILING DATE:  19930524
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/891,543
;      FILING DATE:  29 MAY 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Thomas D. Brainard
;      REGISTRATION NUMBER:  32,459
;      REFERENCE/DOCKET NUMBER:  5172.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-4884
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid (synthetic DNA)
PCT-US93-04863-27


  Query Match             91.7%;  Score 22;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggca 22
          ||||||||||||||||||||||
Db     22 CTCGCAAGCACCCTATCAGGCA 1


RESULT  37
US-08-738-928-3
; Sequence 3, Application US/08738928
; Patent No. 5837442
;  GENERAL INFORMATION:
;    APPLICANT:  Tsang, Sue Y.
;    TITLE OF INVENTION:  Oligonucleotide Primers for Amplifying
;    TITLE OF INVENTION:  HCV Nucleic Acid
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,928
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  9263
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-738-928-3
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```
  Query Match             87.5%;  Score 21;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.00023;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gcaagcacccctatcaggcagt 24
          |||||||||||||||||||||
Db      1 GCAAGCACCCTATCAGGCAGT 21


RESULT  38
US-08-738-928-2
; Sequence 2, Application US/08738928
; Patent No. 5837442
;  GENERAL INFORMATION:
;    APPLICANT:  Tsang, Sue Y.
;    TITLE OF INVENTION:  Oligonucleotide Primers for Amplifying
;    TITLE OF INVENTION:  HCV Nucleic Acid
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,928
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  9263
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-738-928-2


  Query Match             87.5%;  Score 21;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00023;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gcaagcacccctatcaggcagt 24
          |||||||||||||||||||||
Db      1 GCAAGCACCCTATCAGGCAGT 21


RESULT  39
US-09-039-866-4
; Sequence 4, Application US/09039866
; Patent No. 6001611
;  GENERAL INFORMATION:
;    APPLICANT:  Will, Stephen G.
;    TITLE OF INVENTION:  MODIFIED NUCLEIC ACID AMPLIFICATION
;    TITLE OF INVENTION:  PRIMERS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Roche Molecular Systems
;      STREET:  1080 U.S. Highway 202
;      CITY:  Branchburg
;      STATE:  New Jersey
;      COUNTRY:  United States
;      ZIP:  08876
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/039,866
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  1023P
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-039-866-4


  Query Match             87.5%;  Score 21;  DB 3;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00023;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gcaagcacccctatcaggcagt 24
          |||||||||||||||||||||
Db      1 GCAAGCACCCTATCAGGCAGT 21


RESULT  40
US-08-474-700B-35/c
; Sequence 35, Application US/08474700B
; Patent No. 6001990
;  GENERAL INFORMATION:
;    APPLICANT:  Wands, Jack
;    APPLICANT:  Wakita, Takaji
;    APPLICANT:  Moradpour, Darius
;    TITLE OF INVENTION:  ANTISENSE INHIBITION OF HEPATITIS C
;    TITLE OF INVENTION:  VIRUS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,700B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,382
;      FILING DATE:  10 May 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/279001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  35:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-474-700B-35


  Query Match             87.5%;  Score 21;  DB 3;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00023;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggc 21
           |||||||||||||||||||||
Db      21 CTCGCAAGCACCCTATCAGGC 1


RESULT  41
PCT-US95-05812-35/c
; Sequence 35, Application PC/TUS9505812
;  GENERAL INFORMATION:
;    APPLICANT:  Wakita, Takaji
;    APPLICANT:  Wands, Jack
;    TITLE OF INVENTION:  ANTISENSE INHIBITION OF
;    TITLE OF INVENTION:  HEPATITIS C VIRUS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05812
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,382
;      FILING DATE:  10 May 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/221001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-05812-35


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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggc 21
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Db      21 CTCGCAAGCACCCTATCAGGC 1


Search completed: August 26, 2002, 22:17:12
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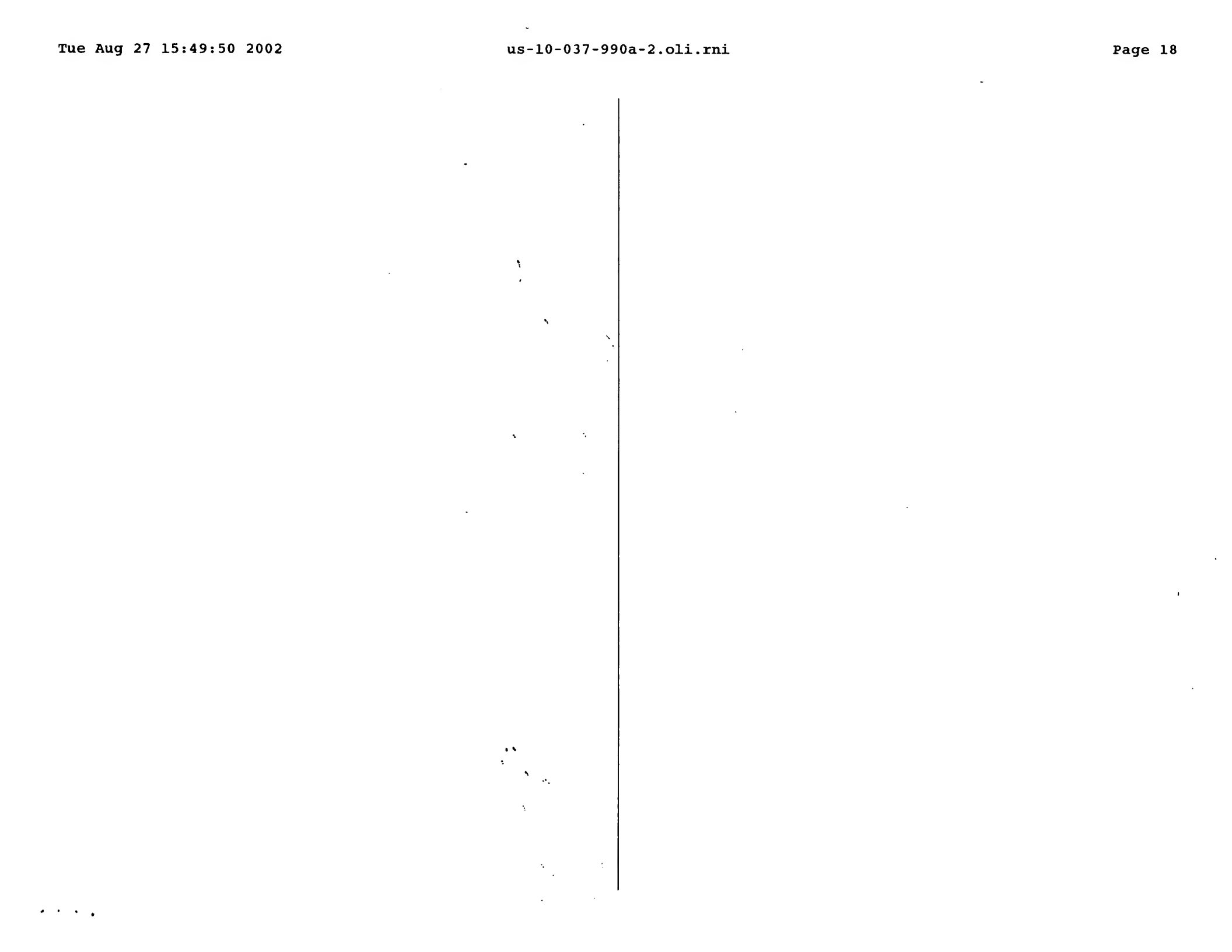
Job time: 5905 sec



GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:14:58 ; Search time 3233.25 Seconds
(without alignments)
100.186 Million cell updates/sec

Title: US-10-037-990A-2
Perfect score: 24
Sequence: 1 ctcgcaagcaccctatcaggcagt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 21:20:52 ; Search time 1915.63 Seconds
(without alignments)
262.178 Million cell updates/sec

Title: US-10-037-990A-2
Perfect score: 24
Sequence: 1 ctcgcaagcaccctatcaggcagt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 54

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
	1	24	100.0	24	6	A68286	A68286 Sequence 7
c	2	24	100.0	24	6	AR011642	AR011642 Sequence
	3	24	100.0	24	6	AR054579	AR054579 Sequence
	4	24	100.0	24	6	AX003942	AX003942 Sequence
	5	24	100.0	24	6	AX021564	AX021564 Sequence
	6	24	100.0	24	6	AX021623	AX021623 Sequence
c	7	24	100.0	24	6	AX040437	AX040437 Sequence
	8	24	100.0	24	6	AX147012	AX147012 Sequence
	9	24	100.0	24	6	I22159	I22159 Sequence 18
	10	24	100.0	24	6	I26948	I26948 Sequence 16
	11	24	100.0	24	6	I40300	I40300 Sequence 8
	12	24	100.0	24	6	I59677	I59677 Sequence 8
	13	24	100.0	24	6	I68635	I68635 Sequence 8
	14	24	100.0	26	6	A39032	A39032 Sequence 4
	15	24	100.0	26	6	AR063366	AR063366 Sequence
	16	24	100.0	26	6	AR123557	AR123557 Sequence
	17	24	100.0	26	6	AX023094	AX023094 Sequence
	18	24	100.0	26	6	E50770	E50770 Vector expr
	19	24	100.0	26	6	I22160	I22160 Sequence 19
	20	24	100.0	27	6	AX202931	AX202931 Sequence
	21	24	100.0	27	6	AX202933	AX202933 Sequence
c	22	24	100.0	27	6	AX282438	AX282438 Sequence
	23	24	100.0	27	6	BD000268	BD000268 Oligonucl
	24	24	100.0	28	6	AR094974	AR094974 Sequence
	25	24	100.0	33	6	AR004397	AR004397 Sequence
	26	24	100.0	33	6	AR064936	AR064936 Sequence
	27	24	100.0	33	6	AR097189	AR097189 Sequence
	28	24	100.0	33	6	AR130687	AR130687 Sequence
	29	24	100.0	33	6	AR172036	AR172036 Sequence
	30	24	100.0	33	6	I82872	I82872 Sequence 51
	31	24	100.0	40	6	E17189	E17189 Partial seq
c	32	24	100.0	47	6	AX284180	AX284180 Sequence
	33	24	100.0	53	6	I44587	I44587 Sequence 16
	34	24	100.0	53	6	I44620	I44620 Sequence 49
	35	24	100.0	53	6	I70992	I70992 Sequence 16
	36	24	100.0	53	6	I71025	I71025 Sequence 49
c	37	24	100.0	57	6	I73305	I73305 Sequence 36
c	38	24	100.0	59	6	AX003948	AX003948 Sequence
c	39	24	100.0	59	6	AX021624	AX021624 Sequence
	40	24	100.0	64	6	I44602	I44602 Sequence 31
	41	24	100.0	64	6	I71007	I71007 Sequence 31
c	42	24	100.0	75	6	AX021668	AX021668 Sequence
	43	23	95.8	23	6	I73294	I73294 Sequence 25
	44	23	95.8	29	6	I22161	I22161 Sequence 20
c	45	22	91.7	22	6	I73296	I73296 Sequence 27
	46	22	91.7	24	6	AX250665	AX250665 Sequence
	47	21	87.5	25	6	AX250673	AX250673 Sequence
	48	21	87.5	27	6	AR054577	AR054577 Sequence
	49	21	87.5	27	6	BD000267	BD000267 Oligonucl
	50	21	87.5	28	6	AR054576	AR054576 Sequence
	51	21	87.5	28	6	AR094138	AR094138 Sequence
c	52	21	87.5	28	6	AR094997	AR094997 Sequence
	53	21	87.5	28	6	AX147022	AX147022 Sequence
	54	21	87.5	46	6	E58845	E58845 Method for

ALIGNMENTS

RESULT 1
A68286
LOCUS A68286 24 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 7 from Patent WO9746716.
ACCESSION A68286
VERSION A68286.1 GI:4759407
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Bosio,P., Strumia,C. and Clemenza,F.
TITLE METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS
JOURNAL Patent: WO 9746716-A 7 11-DEC-1997;

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          WABCO B V (NL)
COMMENT     Other publication IT RM960404 19971209.
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   2
AR011642/c
LOCUS       AR011642                 24 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 51 from patent US 5763159.
ACCESSION   AR011642
VERSION     AR011642.1  GI:3969632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Simmonds,P., Chan,S.-W. and Yap,P.Lee.
  TITLE     Hepatitis-C virus testing
  JOURNAL   Patent: US 5763159-A 51 09-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        4 a      5 c      9 g      6 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     24 CTCGCAAGCACCCTATCAGGCAGT 1


RESULT   3
AR054579
LOCUS       AR054579                 24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5837442.
ACCESSION   AR054579
VERSION     AR054579.1  GI:5980156
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tsang,S.Yen.
  TITLE     Oligonucleotide primers for amplifying HCV nucleic acid
  JOURNAL   Patent: US 5837442-A 5 17-NOV-1998;
FEATURES             Location/Qualifiers
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BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   4
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LOCUS       AX003942                 24 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 2 from Patent WO9923249.
ACCESSION   AX003942
VERSION     AX003942.1  GI:9927602
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kessler,C. and Bartl,K.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923249-A 2 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="KY78"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   5
AX021564
LOCUS       AX021564                 24 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9924606.
ACCESSION   AX021564
VERSION     AX021564.1  GI:10044848
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive nucleic acid detection method
  JOURNAL   Patent: WO 9924606-A 2 20-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:11103"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24
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RESULT   6
AX021623
LOCUS       AX021623                  24 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9923250.
ACCESSION   AX021623
VERSION     AX021623.1  GI:10044906
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923250-A 2 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
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BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   7
AX040437/c
LOCUS       AX040437                  24 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 2 from Patent WO0063444.
ACCESSION   AX040437
VERSION     AX040437.1  GI:11230244
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Budkowska,A., Maillard,P., Nitkiewicz,J. and Crainic,R.
  TITLE     Method for detecting hepatitis c virus with hybridomas
  JOURNAL   Patent: WO 0063444-A 2 26-OCT-2000;
            INSTITUT PASTEUR (FR)
FEATURES             Location/Qualifiers
     source          1. .24
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                     /db_xref="taxon:11103"
BASE COUNT        4 a      5 c      9 g      6 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     24 CTCGCAAGCACCCTATCAGGCAGT 1


RESULT   8
AX147012
LOCUS       AX147012                  24 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 6 from Patent WO0137291.
ACCESSION   AX147012
VERSION     AX147012.1  GI:14346283
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Weindel,K., Riedling,M. and Geiger,A.
  TITLE     Magnetic glass particles, method for their preparation and uses
            thereof
  JOURNAL   Patent: WO 0137291-A 6 25-MAY-2001;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
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                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide primer (HCV reverse)"
     misc_feature    1
                     /note="Biotin derivatization"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT   9
I22159
LOCUS       I22159                    24 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 18 from patent US 5527669.
ACCESSION   I22159
VERSION     I22159.1  GI:1602513
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Resnick,R.M. and Young,K.K.Y.
  TITLE     Methods, primers and probes for detection of hepatitis C and novel
            variants
  JOURNAL   Patent: US 5527669-A 18 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT  10
I26948
LOCUS       I26948                    24 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 16 from patent US 5561058.
ACCESSION   I26948
VERSION     I26948.1  GI:1606818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Gelfand,D.H., Myers,T.W. and Sigua,C.L.
```

```
  TITLE     Methods for coupled high temperatures reverse transcription and
            polymerase chain reactions
  JOURNAL   Patent: US 5561058-A 16 01-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


  Query Match           100.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT  11
I40300
LOCUS       I40300                  24 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 8 from patent US 5620852.
ACCESSION   I40300
VERSION     I40300.1  GI:2082592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Lin,L., Cimino,G. and Zhu,Y.S.
  TITLE     Nucleic acid preparation methods
  JOURNAL   Patent: US 5620852-A 8 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


  Query Match           100.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT  12
I59677
LOCUS       I59677                  24 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 8 from patent US 5654179.
ACCESSION   I59677
VERSION     I59677.1  GI:2478309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Lin,L.
  TITLE     Nucleic acid preparation methods
  JOURNAL   Patent: US 5654179-A 8 05-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


  Query Match           100.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT  13
I68635
LOCUS       I68635                  24 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 8 from patent US 5677124.
ACCESSION   I68635
VERSION     I68635.1  GI:2830757
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   DuBois,D.B., Winkler,M.M. and Pasloske,B.L.
  TITLE     Ribonuclease resistant viral RNA standards
  JOURNAL   Patent: US 5677124-A 8 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      9 c      5 g      4 t
ORIGIN


  Query Match           100.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 0.00034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 CTCGCAAGCACCCTATCAGGCAGT 24


RESULT  14
A39032
LOCUS       A39032                  26 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 4 from Patent WO9412670.
ACCESSION   A39032
VERSION     A39032.1  GI:2295418
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Maertens,G., Stuyver,L., Rossau,R. and Van,H.H.
  TITLE     PROCESS FOR TYPING OF HCV ISOLATES
  JOURNAL   Patent: WO 9412670-A 4 09-JUN-1994;
            INNOGENETICS NV (BE)
COMMENT     Other publication AU 5628294 940622
            Other publication CA 2128528 940609
            Other publication JP 7503143T 950406.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      10 c      5 g      4 t
ORIGIN


  Query Match           100.0%;  Score 24;  DB 6;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  15
AR063366
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LOCUS       AR063366                  26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5846704.
ACCESSION   AR063366
VERSION     AR063366.1  GI:5992674
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
  TITLE     Process for typing of HCV isolates
  JOURNAL   Patent: US 5846704-A 4 08-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        7 a      10 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  16
AR123557
LOCUS       AR123557                  26 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6171784.
ACCESSION   AR123557
VERSION     AR123557.1  GI:14108918
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
  TITLE     Process for typing of HCV isolates
  JOURNAL   Patent: US 6171784-A 4 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        7 a      10 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  17
AX023094
LOCUS       AX023094                  26 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 4 from Patent EP0905258.
ACCESSION   AX023094
VERSION     AX023094.1  GI:10046559
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   .
  TITLE     Method for detecting nucleic acid sequences based on the use of
            solid phase immobilised nucleotide probes (line probe assay)
  JOURNAL   Patent: EP 0905258-A 4 31-MAR-1999;
            INNOGENETICS NV (BE)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Hepatitis C virus"
                     /isolate="HCV"
                     /db_xref="taxon:11103"
                     /map="POSITION -29 OF 5' END"
     misc_feature    1. .26
                     /standard_name="UNIVERSAL HCV PRIMER HCPR96"
BASE COUNT        7 a      10 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  18
E50770
LOCUS       E50770                    26 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Vector expressing full-length gene of RNA virus and utilization
            thereof.
ACCESSION   E50770
VERSION     E50770.1  GI:18628195
KEYWORDS    JP 2000152793-A/23.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.
  TITLE     Vector expressing full-length gene of RNA virus and utilization
  JOURNAL   Patent: JP 2000152793-A 23 06-JUN-2000;
            TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI
            PHARMACEUT CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000152793-A/23
            PD   06-JUN-2000
            PF   24-JUN-1999 JP 1999178347
            PR
            PI   MICHINORI OBARA,KYOKO OBARA,KAZUNARI TABIRA,JUNICHI MATSUZAKI,
            PI   HIROSHI OMORI
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        7 a      10 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  19
I22160
LOCUS       I22160                    26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 19 from patent US 5527669.
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ACCESSION   I22160
VERSION     I22160.1  GI:1602514
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Resnick,R.M. and Young,K.K.Y.
  TITLE     Methods, primers and probes for detection of hepatitis C and novel
            variants
  JOURNAL   Patent: US 5527669-A 19 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        7 a      10 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  20
AX202931
LOCUS       AX202931                  27 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 6 from Patent WO0152612.
ACCESSION   AX202931
VERSION     AX202931.1  GI:15392394
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Elaissari,A., Mandrand,B., Delair,T., Spencer,D. and Arkis,A.
  TITLE     Method for isolating proteins or protein and nucleic acid
            associations, or particle and protein complexes, reagent and uses
  JOURNAL   Patent: WO 0152612-A 6 26-JUL-2001;
            BIO MERIEUX (FR)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unidentified"
                     /db_xref="taxon:32644"
                     /note="Origine de la sequence :AMORCE"
BASE COUNT        8 a      10 c       5 g       4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      2 CTCGCAAGCACCCTATCAGGCAGT 25


RESULT  21
AX202933
LOCUS       AX202933                  27 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 8 from Patent WO0152612.
ACCESSION   AX202933
VERSION     AX202933.1  GI:15392396
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Elaissari,A., Mandrand,B., Delair,T., Spencer,D. and Arkis,A.
  TITLE     Method for isolating proteins or protein and nucleic acid
            associations, or particle and protein complexes, reagent and uses
  JOURNAL   Patent: WO 0152612-A 8 26-JUL-2001;
            BIO MERIEUX (FR)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unidentified"
                     /db_xref="taxon:32644"
                     /note="Origine de la sequence :AMORCE"
BASE COUNT        8 a      10 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      2 CTCGCAAGCACCCTATCAGGCAGT 25


RESULT  22
AX282438/c
LOCUS       AX282438                  27 bp    mRNA    linear   PAT 02-NOV-2001
DEFINITION  Sequence 10 from Patent WO0166721.
ACCESSION   AX282438
VERSION     AX282438.1  GI:16609569
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Usman,N., Mcswiggen,J.A., Zinnen,S., Seiwert,S., Haeberli,P.,
            Chowrira,B. and Blatt,L.
  TITLE     Nucleic acid sensor molecules
  JOURNAL   Patent: WO 0166721-A 10 13-SEP-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic target signaling sequence"
BASE COUNT        4 a      5 c       10 g      8 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     25 CTCGCAAGCACCCTATCAGGCAGT 2


RESULT  23
BD000268
LOCUS       BD000268                  27 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Oligonucleotide primers for efficient detection of hepatitis C
            virus (HCV) and methods of use thereof.
ACCESSION   BD000268
VERSION     BD000268.1  GI:18623347
KEYWORDS    JP 2000279200-A/6.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lynen,J.M. and Gorman,K.M.
  TITLE     Oligonucleotide primers for efficient detection of hepatitis C
            virus (HCV) and methods of use thereof
  JOURNAL   Patent: JP 2000279200-A 6 10-OCT-2000;
            ORTHO CLINICAL DIAGNOSTICS INC
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COMMENT     OS   Artificial Sequence
            PN   JP 2000279200-A/6
            PD   10-OCT-2000
            PF   03-FEB-2000 JP 2000032656
            PR   03-FEB-1999 US    60/118497
            PI   JEFFREY M LYNEN,KEVIN M GORMAN
            PC   C12Q1/68,C12N15/09//(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
            PC   C12R1:92)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .27
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      10 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 CTCGCAAGCACCCTATCAGGCAGT 26


RESULT  24
AR094974
LOCUS       AR094974                  28 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 12 from patent US 6001990.
ACCESSION   AR094974
VERSION     AR094974.1  GI:10022401
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wands,J.R., Wakita,T. and Moradpour,D.
  TITLE     Antisense inhibition of hepatitis C virus
  JOURNAL   Patent: US 6001990-A 12 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        8 a      11 c       5 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      2 CTCGCAAGCACCCTATCAGGCAGT 25


RESULT  25
AR004397
LOCUS       AR004397                  33 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 51 from patent US 5747244.
ACCESSION   AR004397
VERSION     AR004397.1  GI:3965276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Sheridan,P., Chang,C.-A., Running,J. and Urdea,M.S.
  TITLE     Nucleic acid probes immobilized on polystyrene surfaces
  JOURNAL   Patent: US 5747244-A 51 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      12 c       9 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  26
AR064936
LOCUS       AR064936                  33 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 61 from patent US 5849481.
ACCESSION   AR064936
VERSION     AR064936.1  GI:5995152
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Urdea,M.S., Horn,T., Chang,C.-A., Warner,B. and Fultz,T.J.
  TITLE     Nucleic acid hybridization assays employing large comb-type
            branched polynucleotides
  JOURNAL   Patent: US 5849481-A 61 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      12 c       9 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  27
AR097189
LOCUS       AR097189                  33 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 127 from patent US 6071693.
ACCESSION   AR097189
VERSION     AR097189.1  GI:12805919
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Cha,T., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
  TITLE     HCV genomic sequences for diagnostics and therapeutics
  JOURNAL   Patent: US 6071693-A 127 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      12 c       9 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
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          ||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  28
AR130687
LOCUS       AR130687                  33 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 127 from patent US 6190864.
ACCESSION   AR130687
VERSION     AR130687.1  GI:14119012
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Cha,T., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
  TITLE     HCV genomic sequences for diagnostics and therapeutics
  JOURNAL   Patent: US 6190864-A 127 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      12 c       9 g       4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  29
AR172036
LOCUS       AR172036                  33 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 127 from patent US 6297370.
ACCESSION   AR172036
VERSION     AR172036.1  GI:17910986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
  TITLE     HCV genomic sequences for diagnostics and therapeutics
  JOURNAL   Patent: US 6297370-A 127 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      12 c       9 g       4 t
ORIGIN


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Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  30
I82872
LOCUS       I82872                    33 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 51 from patent US 5712383.
ACCESSION   I82872
VERSION     I82872.1  GI:3211169
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Sheridan,P., Chang,C.-A., Running,J. and Urdea,M.S.
  TITLE     Process for immobilizing nucleic acid probes on polystyrene
            surfaces
  JOURNAL   Patent: US 5712383-A 51 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      12 c       9 g       4 t
ORIGIN


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Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 CTCGCAAGCACCCTATCAGGCAGT 30


RESULT  31
E17189
LOCUS       E17189                    40 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Partial sequence of HCV gene.
ACCESSION   E17189
VERSION     E17189.1  GI:5711872
KEYWORDS    JP 1998248579-A/3.
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Obara,M., Inoue,K., Katsume,A., Takeuchi,T. and Kawaguchi,R.
  TITLE     MEASUREMENT OF HCV GENE BY REAL TIME DETECTION PCR METHOD, AND
            PRIMER AND PROBE TO BE USED THEREFOR
  JOURNAL   Patent: JP 1998248579-A 3 22-SEP-1998;
            TOKYO MET GOV RINSHIYOU IGAKU SOGO KENKYUSHO, S R L:KK
COMMENT     OS   Hepatitis C virus
            PN   JP 1998248579-A/3
            PD   22-SEP-1998
            PF   05-MAR-1997 JP 1997067321
            PI   OBARA MICHINORI, INOUE KAZUAKI, KATSUME ASAO, TAKEUCHI TOMOKO,
            PI   KAWAGUCHI RYUJI
            PC   C12N15/09,C07H21/02,C07H21/04,C12Q1/68,G01N33/566,G01N33/576;
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .40
            FT                   /organism='Hepatitis C virus'.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT        9 a      17 c       9 g       5 t
ORIGIN


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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     13 CTCGCAAGCACCCTATCAGGCAGT 36


RESULT  32
AX284180/c
LOCUS       AX284180                  47 bp    DNA     linear   PAT 20-NOV-2001
DEFINITION  Sequence 1 from Patent WO0179420.
```

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ACCESSION   AX284180
VERSION     AX284180.1  GI:17044868
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Faruqi,A.F.
  TITLE     Detection and amplification or rna using target-mediated ligation
            of dna by rna ligase
  JOURNAL   Patent: WO 0179420-A 1 25-OCT-2001;
            MOLECULAR STAGING, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Target"
BASE COUNT        7 a     11 c     18 g     11 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.0003;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     39 CTCGCAAGCACCCTATCAGGCAGT 16


RESULT  33
I44587
LOCUS       I44587                   53 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 16 from patent US 5635352.
ACCESSION   I44587
VERSION     I44587.1  GI:2469300
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise
  JOURNAL   Patent: US 5635352-A 16 03-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT       12 a     17 c     15 g      9 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  34
I44620
LOCUS       I44620                   53 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 49 from patent US 5635352.
ACCESSION   I44620
VERSION     I44620.1  GI:2469333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise
  JOURNAL   Patent: US 5635352-A 49 03-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT       12 a     17 c     15 g      9 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  35
I70992
LOCUS       I70992                   53 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 16 from patent US 5681697.
ACCESSION   I70992
VERSION     I70992.1  GI:3007127
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise and kits therefor
  JOURNAL   Patent: US 5681697-A 16 28-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT       12 a     17 c     15 g      9 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  36
I71025
LOCUS       I71025                   53 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 49 from patent US 5681697.
ACCESSION   I71025
VERSION     I71025.1  GI:3007160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise and kits therefor
  JOURNAL   Patent: US 5681697-A 49 28-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT       12 a     17 c     15 g      9 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 53;
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  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 CTCGCAAGCACCCTATCAGGCAGT 50


RESULT  37
I73305/c
LOCUS       I73305                    57 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 36 from patent US 5686272.
ACCESSION   I73305
VERSION     I73305.1  GI:3009444
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 57)
  AUTHORS   Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
  TITLE     Amplification of RNA sequences using the ligase chain reaction
  JOURNAL   Patent: US 5686272-A 36 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="unknown"
BASE COUNT        9 a      9 c     23 g     16 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     57 CTCGCAAGCACCCTATCAGGCAGT 34


RESULT  38
AX003948/c
LOCUS       AX003948                  59 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 8 from Patent WO9923249.
ACCESSION   AX003948
VERSION     AX003948.1  GI:9927608
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Kessler,C. and Bartl,K.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923249-A 8 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE)
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT        9 a     16 c     21 g     13 t
ORIGIN


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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     26 CTCGCAAGCACCCTATCAGGCAGT 3


RESULT  39
AX021624/c
LOCUS       AX021624                  59 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9923250.
ACCESSION   AX021624
VERSION     AX021624.1  GI:10044907
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923250-A 3 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT        9 a     16 c     21 g     13 t
ORIGIN


  Query Match           100.0%;  Score 24;  DB 6;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     26 CTCGCAAGCACCCTATCAGGCAGT 3


RESULT  40
I44602
LOCUS       I44602                    64 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 31 from patent US 5635352.
ACCESSION   I44602
VERSION     I44602.1  GI:2469315
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise
  JOURNAL   Patent: US 5635352-A 31 03-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="unknown"
BASE COUNT       18 a     16 c     17 g     13 t
ORIGIN


  Query Match           100.0%;  Score 24;  DB 6;  Length 64;
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Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     23 CTCGCAAGCACCCTATCAGGCAGT 46


RESULT  41
I71007
LOCUS       I71007                    64 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 31 from patent US 5681697.
ACCESSION   I71007
VERSION     I71007.1  GI:3007142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 64)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise and kits therefor
  JOURNAL   Patent: US 5681697-A 31 28-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="unknown"
BASE COUNT       18 a     16 c     17 g     13 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.00028;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     23 CTCGCAAGCACCCTATCAGGCAGT 46


RESULT  42
AX021668/c
LOCUS       AX021668                  75 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 47 from Patent WO9923250.
ACCESSION   AX021668
VERSION     AX021668.1  GI:10044951
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 75)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923250-A 47 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis C virus"
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ORIGIN


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Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     33 CTCGCAAGCACCCTATCAGGCAGT 10


RESULT  43
I73294
LOCUS       I73294                    23 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 25 from patent US 5686272.
ACCESSION   I73294
VERSION     I73294.1  GI:3009433
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
  TITLE     Amplification of RNA sequences using the ligase chain reaction
  JOURNAL   Patent: US 5686272-A 25 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT        6 a      8 c      5 g      4 t
ORIGIN


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  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          |||||||||||||||||||||||
Db      1 TCGCAAGCACCCTATCAGGCAGT 23


RESULT  44
I22161
LOCUS       I22161                    29 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 20 from patent US 5527669.
ACCESSION   I22161
VERSION     I22161.1  GI:1602515
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Resnick,R.M. and Young,K.K.Y.
  TITLE     Methods, primers and probes for detection of hepatitis C and novel
            variants
  JOURNAL   Patent: US 5527669-A 20 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        8 a      8 c      8 g      5 t
ORIGIN


  Query Match           95.8%;  Score 23;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.0014;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          |||||||||||||||||||||||
Db      7 TCGCAAGCACCCTATCAGGCAGT 29


RESULT  45
I73296/c
LOCUS       I73296                    22 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 27 from patent US 5686272.
ACCESSION   I73296
VERSION     I73296.1  GI:3009435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
  TITLE     Amplification of RNA sequences using the ligase chain reaction
  JOURNAL   Patent: US 5686272-A 27 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        3 a      4 c      9 g      6 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.0061;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggca 22
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Db     22 CTCGCAAGCACCCTATCAGGCA 1
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Perfect score: 24
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	24	100.0	24	14	AAQ43144	HCV core region re
	2	24	100.0	24	14	AAQ37586	HCV conserved regi
	3	24	100.0	24	16	AAQ79963	Primer KY78 for HC
	4	24	100.0	24	18	AAT64900	Hepatitis C virus
	5	24	100.0	24	18	AAT93542	Antisense primer K
	6	24	100.0	24	18	AAT87095	HCV gene PCR prime
	7	24	100.0	24	19	AAV18850	Primer KY78 for HC
	8	24	100.0	24	19	AAV15319	Hepatitis C virus
	9	24	100.0	24	20	AAZ09798	HCV PCR primer KY7
	10	24	100.0	24	20	AAX78452	HCV PCR primer 2.
	11	24	100.0	24	20	AAX23969	PCR primer KY78.
c	12	24	100.0	24	21	AAC66753	PCR primer #2 used
	13	24	100.0	24	22	AAH25404	PCR primer used to
	14	24	100.0	26	14	AAQ37587	HCV conserved regi
	15	24	100.0	26	15	AAQ68061	Primer HcPr96 for
	16	24	100.0	26	18	AAT64901	Hepatitis C virus
	17	24	100.0	26	21	AAZ57408	Hepatitis C virus
	18	24	100.0	27	15	AAQ71839	PCR primer for hep
	19	24	100.0	27	21	AAA74624	HCV-specific ampli
	20	24	100.0	27	21	AAZ87367	Hepatitis C virus
	21	24	100.0	27	22	ABA02736	Nucleic acid senso
c	22	24	100.0	27	22	ABA02738	Nucleic acid senso
	23	24	100.0	27	22	AAH78439	PCR primer used to
	24	24	100.0	27	22	AAH78441	PCR primer used to
	25	24	100.0	27	23	ABK09262	Enzymatic nucleic
c	26	24	100.0	27	23	ABK09264	Enzymatic nucleic
	27	24	100.0	28	16	AAT05222	Hepatitis C virus
	28	24	100.0	28	21	AAZ57757	Hepatitis C virus
	29	24	100.0	30	15	AAQ55728	Hepatitis C detect
	30	24	100.0	33	13	AAQ31158	Probe 127 for geno
	31	24	100.0	33	14	AAQ46464	Hepatitis C virus
	32	24	100.0	33	19	AAV07838	HCV.33.9 amplifier
	33	24	100.0	33	20	AAV83066	Amplifier probe HC
	34	24	100.0	40	19	AAV54436	Nucleotide sequenc
	35	24	100.0	53	16	AAQ98139	Control label exte
	36	24	100.0	53	16	AAQ98104	Label extender pro
c	37	24	100.0	57	14	AAQ63223	Hepatitis C virus
c	38	24	100.0	59	20	AAZ23543	HCV DNA fragment 2
c	39	24	100.0	59	20	AAZ09795	HCV DNA probe. Sy
	40	24	100.0	64	16	AAQ98121	Label extender pro
	41	23	95.8	23	14	AAQ53257	Hepatitis C virus
	42	23	95.8	29	14	AAQ37588	HCV conserved regi
	43	23	95.8	29	18	AAT64902	Hepatitis C virus
c	44	22	91.7	22	14	AAQ53259	Hepatitis C virus
	45	22	91.7	23	24	AAD25564	HCV RNA 5' UTR amp
	46	22	91.7	23	24	AAD25666	Oligonucleotide #1
	47	22	91.7	24	22	AAD19057	Hepatitis viral DN
c	48	22	91.7	52	21	AAA29435	Hepatitis C virus
	49	21	87.5	25	22	AAH79082	HCV PCR primer SEQ
	50	21	87.5	27	18	AAT67195	Hepatitis C virus
	51	21	87.5	27	21	AAA74623	HCV-specific ampli
c	52	21	87.5	28	16	AAT05245	Hepatitis C virus
	53	21	87.5	28	18	AAT67194	Hepatitis C virus
	54	21	87.5	28	19	AAV59059	Primer ST778AA for
c	55	21	87.5	28	21	AAZ57785	Hepatitis C virus
	56	21	87.5	28	22	AAH25414	Reverse PCR primer
	57	21	87.5	46	22	AAF58265	Hepatitis C virus

ALIGNMENTS

RESULT 1
AAQ43144/c
ID AAQ43144 standard; DNA; 24 BP.
XX
AC AAQ43144;
XX
DT 23-SEP-1993 (first entry)
XX
DE HCV core region reverse transcription primer #2.
XX
KW Non-coding region; hepatitis C virus; blood donor; type 2; type 1;
KW HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3;
KW PCR; amplify; polymerase chain reaction; primer; NS4; ss.
XX
OS Synthetic.
XX
PN WO9310239-A.
XX
PD 27-MAY-1993.
XX

PF 20-NOV-1992; 92WO-GB02143.
XX
PR 21-NOV-1991; 91GB-0024696.
PR 24-JUN-1992; 92GB-0013362.
XX
PA (COMM-) COMMON SERVICES AGENCY.
XX
PI Chan S, Simmonds P, Yap PL;
XX
DR WPI; 1993-182554/22.
XX
PT DNA encoding antigenic peptide(s) of new types of hepatitis C
PT virus - for diagnosing and treating HCV infection, screening
PT blood samples and identifying different HCV types
XX
PS Disclosure; Page 44; 120pp; English.
XX
CC The sequences given in AAQ43143-46 are primers which were used to
CC reverse transcribe the core region of the hepatitis C virus (HCV)
CC genome for sequence analysis. Analysis of regions of the HCV genome
CC revealed the existance of three distinct groups of HCV. Analysis of
CC the region encompassing -255 to -62 of the 5' non coding region (NCR)
CC (see AAQ43058-75) showed a difference of 9-14% in the nucleotide
CC sequences between the three groups. Two of the groups identified
CC were similar to those of HCV varients termed type 1 and 2, whilst the
CC third appeared to represent a novel type of virus. Comparison of the
CC NS3 region (see AAR37927-30) showed a high degree of sequence diversity
CC with type 3 being phylogenetically different to type 1 and 2. The
CC same degree differentiation was noted in the NS-5 (see AAR37923-26),
CC core region (see AAR37931) and the NS4 region (see AAQ43106-111) between
CC type 3 and type 1 sequences.
XX
SQ Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 24 CTCGCAAGCACCCTATCAGGCAGT 1

RESULT 2
AAQ37586
ID AAQ37586 standard; DNA; 24 BP.
XX
AC AAQ37586;
XX
DT 23-JUN-1993 (first entry)
XX
DE HCV conserved region downstream primer/probe KY78, position 276-299.
XX
KW Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW regulation; US; Japan; C9; ss.
XX
OS Synthetic.
XX
PN EP529493-A.
XX
PD 03-MAR-1993.
XX
PF 19-AUG-1992; 92EP-0114115.
XX
PR 27-AUG-1991; 91US-0751305.
PR 21-JUL-1992; 92US-0918844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Resnick RM, Young KKY;
XX
DR WPI; 1993-068572/09.
XX
PT Compsn. comprising oligo:nucleotide probe-primer - used for
PT detecting hepatitis C virus strains Japan, US and C9
XX
PS Claim 3; Page 8; 43pp; English.
XX
CC The sequences given in AAQ37569-96 are oligonucleotides which can be
CC used as primers or probes which hybridise to the conserved region at
CC the 5'-end of the hepatitis C virus (HCV) genome. HCV is a small
CC RNA virus containing a small, positive sense, molecule of RNA about
CC 10,000 nucleotides in length. the genome contains a single, long,
CC open reading frame believed to translated in to a single, large
CC polyprotein and subsequently processed. The open reading frame
CC begins at nucleotide 343 (using the numbering system from the
CC prototype virus) following an untranslated region (UTR) the 5'UTR
CC sequence is relatively conserved and may be important in viral
CC replication and regulation. The 5' end of the coding region is also
CC conserved. These primer/probes can be used to identify different HCV
CC isolates such as US, Japan and C9 (see also AAQ37597-601).
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 1 ctcgcaagcaccctatcaggcagt 24

RESULT 3
AAQ79963
ID AAQ79963 standard; DNA; 24 BP.
XX
AC AAQ79963;
XX
DT 01-AUG-1995 (first entry)
XX
DE Primer KY78 for HCV RNA.
XX
KW Primer; PCR; polymerase chain reaction; amplification;
KW RNA detection; reverse transcription; hepatitis C virus; HCV;
KW ss.
XX
OS Synthetic.
XX
PN EP632134-A.
XX
PD 04-JAN-1995.
XX
PF 20-JUN-1994; 94EP-0109468.
XX
PR 01-JUL-1993; 93US-0086483.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Gelfand DH, Myers TW, Sigua CL;
XX
DR WPI; 1995-037815/06.
XX
PT Improved amplification method for target RNA - using buffering
PT agent which buffers both pH and divalent cation concn.
XX
PS Example 6; Page 22; 37pp; English.
XX
CC The primers given in AAQ79963-64 were used to amplify HCV templates
CC for use in a novel method of RNA amplification involving
CC high-temp. reverse transcription and PCR.
XX

```
SQ   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 16;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 ctcgcaagcaccctatcaggcagt 24


RESULT   4
AAT64900
ID   AAT64900 standard; DNA; 24 BP.
XX
AC   AAT64900;
XX
DT   12-MAR-1998  (first entry)
XX
DE   Hepatitis C virus (HCV) oligonucleotide KY78.
XX
KW   Hepatitis C virus; reverse transcription; probe; PCR primer;
KW   detection; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   EP787807-A2.
XX
PD   06-AUG-1997.
XX
PF   19-AUG-1992;   92EP-0065347.
XX
PR   21-JUL-1992;   92US-0918844.
PR   27-AUG-1991;   91US-0751305.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Resnick RM,  Young KKY;
XX
DR   WPI; 1997-387489/36.
XX
PT   Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT   nucleic acid - from many different strains without loss of
PT   specificity, allow single step reverse transcription and
PT   amplification
XX
PS   Claims 4 and 5; Page 8; 35pp; English.
XX
CC   This oligonucleotide KY78 can be used as a probe for detecting
CC   hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC   strain as well as HCV C9 prototype strain. This oligonucleotide can
CC   also be used as a primer for amplifying HCV nucleic acid. The sequence
CC   of this oligonucleotide is contained in a specific region of HCV genomic
CC   nucleic acid. The probe or the primer is preferably labelled. The probe
CC   is used to detect HCV nucleic acid, preferably after this has been
CC   amplified using the new primer in reverse transcription polymerase chain
CC   reaction (RT-PCR), for both diagnostic and epidemiological applications.
CC   The primer is effective for both reverse transcription and PCR,
CC   eliminating the need to open the reaction tube during the procedure.
CC   Amplification is effective (no need for a second round of PCR with nested
CC   primers) and provides high sensitivity.  The probe is directed to
CC   conserved regions and so can detect many different strains without loss
CC   of specificity.
XX
SQ   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 18;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 ctcgcaagcaccctatcaggcagt 24


RESULT   5
AAT93542
ID   AAT93542 standard; DNA; 24 BP.
XX
AC   AAT93542;
XX
DT   19-FEB-1998  (first entry)
XX
DE   Antisense primer KY78 for amplification of HCV RNA.
XX
KW   Armoured RNA; bacteriophage MS2; RT-PCR; ribonuclease; recombinant;
KW   Human Immunodeficiency virus; HIV; Hepatitis C Virus; HCV; viral RNA;
KW   detection; quantification standard; maturase protein; coat protein;
KW   PCR primer; QS RNA; reverse transcriptase-PCR; ss.
XX
OS   Synthetic.
OS   Hepatitis C Virus.
XX
PN   US5677124-A.
XX
PD   14-OCT-1997.
XX
PF   03-JUL-1996;   96US-0675153.
XX
PR   03-JUL-1996;   96US-0675153.
XX
PA   (AMBI-) AMBION INC.
PA   (CENE-) CENETRON DIAGNOSTICS LLC.
XX
PI   Dubois DB,  Pasloske BL,  Winkler MM;
XX
DR   WPI; 1997-511866/47.
XX
PT   Recombinant RNA segment encapsidated in bacteriophage viral coat
PT   protein - RNA detection and/or quantification standard
XX
PS   Example 5; Column 22; 23pp; English.
XX
CC   This antisense primer is used in the RT-PCR amplification of HCV RNA to
CC   create a quantitative HCV "armoured RNA" standard. An "armoured RNA" is
CC   a recombinant RNA segment encapsidated in bacteriophage viral coat
CC   protein. The recombinant RNA segment comprises an operator coding
CC   sequence, a viral maturase protein binding site, and a non-bacteriophage
CC   sequence. The recombinant RNA in its packaged form is highly resistant to
CC   ribonucleases, insuring that the RNA standard is not compromised by
CC   inadvertent ribonuclease contamination. The armoured RNA standards are
CC   ideal as RNA standards for the quantification of RNA viruses such as HIV
CC   and HCV from human body fluids such as blood and cerebrospinal fluid.
XX
SQ   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 18;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 ctcgcaagcaccctatcaggcagt 24


RESULT   6
AAT87095
ID   AAT87095 standard; DNA; 24 BP.
XX
AC   AAT87095;
XX
DT   07-JAN-1998  (first entry)
```

XX
DE HCV gene PCR primer KY78.
XX
KW RNA; plasma; hepatitis C virus; HCV; primer; PCR;
KW polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN US5654179-A.
XX
PD 05-AUG-1997.
XX
PF 14-NOV-1990; 90US-0614921.
XX
PR 08-APR-1993; 93US-0044649.
PR 14-NOV-1990; 90US-0614921.
PR 19-JUN-1992; 92US-0901545.
PR 03-OCT-1994; 94US-0317220.
XX
PA (HYDS) HRI RES INC.
XX
PI Lin L;
XX
DR WPI; 1997-401849/37.
XX
PT Preparation of RNA samples from plasma - by alcohol precipitation
PT after lysis with guanidinium thiocyanate
XX
PS Disclosure; Column 47; 60pp; English.
XX
CC Primer KY78 (AAT87095) and primer KY80 (AAT87096) were used for the
CC PCR amplification of a 305 bp hepatitis C virus gene product (see
CC AAT87088). A claimed method for preparing RNA samples comprises: (a)
CC mixing plasma with an aqueous buffer solution containing guanidinium
CC thiocyanate and beta-mercaptoethanol; (b) heating the mixture; (c)
CC adding an equal volume of an alcohol to precipitate RNA; and (d)
CC recovering the RNA. The method can be used to prepare RNA samples
CC for subsequent amplification, especially for detecting pathogens,
CC e.g. hepatitis C virus or HIV. Compared with the known ''IsoQuick''
CC and ''RNAzol'' methods, the method uses fewer tubes (just one),
CC requires fewer steps, takes less time and produces no toxic waste.
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 1 ctcgcaagcaccctatcaggcagt 24

RESULT 7
AAV18850
ID AAV18850 standard; DNA; 24 BP.
XX
AC AAV18850;
XX
DT 11-JUN-1998 (first entry)
XX
DE Primer KY78 for HCV DNA.
XX
KW PCR primer; HCV; nucleic acid standard; Armored RNA; ss.
XX
OS Synthetic.
OS Hepatitis virus.
XX
PN WO9800547-A1.
XX
PD 08-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US12551.
XX
PR 24-JUN-1997; 97US-0881571.
PR 03-JUL-1996; 96US-0021145.
PR 03-JUL-1996; 96US-0675153.
XX
PA (AMBI-) AMBION INC.
PA (CENE-) CENETRON DIAGNOSTICS LLC.
XX
PI Dubois DB, Pasloske BL, Winkler MM;
XX
DR WPI; 1998-086972/08.
XX
PT Ribonuclease resistant RNA molecules and their production - useful
PT as standards in quantitative PCR for pathogens, e.g HIV-1, HIV-2 and
PT HCV
XX
PS Example 5; Page 41; 134pp; English.
XX
CC The present sequence is a primer for hepatitis C virus (HCV) DNA,
CC which was used in the preparation of a nucleic acid standard,
CC comprising a nuclease resistant nucleic acid segment encoding a
CC standard nucleic acid, i.e. RNA. The ribonuclease resistant RNA
CC standard, designated Armored RNA (RTM) is useful as an internal or
CC external nucleic acid standard in quantitative assays, e.g. PCR or
CC RT-PCR for the presence of a tested nucleic acid in blood samples.
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 1 ctcgcaagcaccctatcaggcagt 24

RESULT 8
AAV15319
ID AAV15319 standard; DNA; 24 BP.
XX
AC AAV15319;
XX
DT 28-MAY-1998 (first entry)
XX
DE Hepatitis C virus PCR primer PKY78.
XX
KW Hepatitis C virus; HCV; PCR primer; detection; reverse transcription;
KW enzyme immunoassay; viral RNA; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN WO9746716-A1.
XX
PD 11-DEC-1997.
XX
PF 03-JUN-1997; 97WO-IT00128.
XX
PR 07-JUN-1996; 96IT-M000404.
XX
PA (WESA) WABCO BV.
XX
PI Bosio P, Clemenza F, Strumia C;
XX
DR WPI; 1998-042222/04.
XX
PT Detection of hepatitis C virus - by reverse transcription,
PT single-step PCR and detection by DNA enzyme immunoassay
XX
PS Disclosure; Page 4; 26pp; English.

```
XX
CC   The present sequence represents a PCR primer involved in the method of
CC   the present invention for detecting hepatitis C virus (HCV). The method
CC   comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
CC   resulting cDNA by a single polymerase chain reaction in a reaction
CC   mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme
CC   unit; and (c) detecting the amplification product by DEIA (DNA enzyme
CC   immunoassay) using an oligonucleotide probe. The sensitivity of this
CC   method is at least equal to that achievable by more complicated assays
CC   using nested PCR.
XX
SQ   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 19;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 ctcgcaagcaccctatcaggcagt 24


RESULT   9
AAZ09798
ID   AAZ09798 standard; DNA; 24 BP.
XX
AC   AAZ09798;
XX
DT   26-NOV-1999  (first entry)
XX
DE   HCV PCR primer KY78.
XX
KW   Probe; amplification; primer; reporter group; quencher group; PCR;
KW   amplicon; detection; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   DE19814001-A1.
XX
PD   30-SEP-1999.
XX
PF   28-MAR-1998;   98DE-1014001.
XX
PR   28-MAR-1998;   98DE-1014001.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Kessler C,  Haberhausen G,  Batz H,  Orum H;
XX
DR   WPI; 1999-552213/47.
XX
PT   Fluorescent nucleic acid amplification assay, useful for detection of
PT   viral, bacterial, cellular, yeast or fungal nucleic acids  -
XX
PS   Example 1; Page 19; 16pp; German.
XX
CC   This invention describes a novel assay for a nucleic acid which comprises
CC   an amplification reaction using two non-overlapping primers, a polymerase
CC   with 5'-nuclease activity and a probe with reporter groups and quencher
CC   groups that binds a region other than that bound by the primers. The
CC   reaction generates products of less than 100 nucleotides. The assay is
CC   useful for detection of viral, bacterial, cellular, yeast or fungal
CC   nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC   samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC   or liquid biopsy samples. Compared with assays in which longer
CC   amplification products are generated, the assay can be performed more
CC   rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
CC   may be increased due to reduced competition between the short
CC   counterstrand of the amplicon and the detector probe. Specificity may
CC   also be increased because of the increased relative length of sequence B
CC   compared with the total length of the amplicon and the differentiability
CC   of subtypes may be increased. In addition signal-to-noise ratios may be
CC   increased with the new method because short amplicons have reduced
CC   potential for nonspecific hybridization. In addition reproducibility may
CC   be increased because small target regions on RNA genomes are less
CC   sensitive to RNA degradation, and the possibilities for secondary
CC   structure formation are reduced. This sequence represents a PCR primer
CC   used in the amplification of a region of HCV which is used to illustrate
CC   the method of the invention.
XX
SQ   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 ctcgcaagcaccctatcaggcagt 24


RESULT  10
AAX78452
ID   AAX78452 standard; DNA; 24 BP.
XX
AC   AAX78452;
XX
DT   26-AUG-1999  (first entry)
XX
DE   HCV PCR primer 2.
XX
KW   RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
KW   ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV;
KW   HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   US5919625-A.
XX
PD   06-JUL-1999.
XX
PF   29-APR-1997;   97US-0841252.
XX
PR   03-JUL-1996;   96US-0675153.
PR   29-APR-1997;   97US-0841252.
XX
PA   (AMBI-) AMBION INC.
PA   (CENE-) CENETRON DIAGNOSTICS LLC.
XX
PI   Dubois DB,  Pasloske BL,  Winkler MM;
XX
DR   WPI; 1999-394617/33.
XX
PT   Ribonuclease resistant viral RNA standards
XX
PS   Example V; Column 31-32; 22pp; English.
XX
CC   This invention describes the construction of novel RNA standards for the
CC   quantification of human immunodeficiency virus (HIV) and hepatitis C
CC   virus (HCV) from e.g. cerebrospinal fluids. THe method involves (1)
CC   obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
CC   RNA standard, encapsulated in a bacteriophage viral coat protein, which
CC   comprises an RNA segment having a segment encoding a sequence that serves
CC   as a standard in detection or quantification of the RNA of interest;
CC   (3) mixing the sample with the standard; (4) isolating RNA from the
CC   mixture, and (5) assaying for the presence of the RNA. The method is
CC   useful for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1,
CC   HTLV-2, hepatitis G, an enterovirus, or a blood-borne pathogen. This
CC   sequence represents a PCR primer used to amplify a region of the
CC   Hepatitis C genome which is used in the method of the invention.
XX
SQ   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
```

```
  Query Match           100.0%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 ctcgcaagcaccctatcaggcagt 24


RESULT  11
AAX23969
ID   AAX23969 standard; DNA; 24 BP.
XX
AC   AAX23969;
XX
DT   28-JUN-1999  (first entry)
XX
DE   PCR primer KY78.
XX
KW   Amplification; medical; forensic; diagnosis; food analysis; blood;
KW   environmental analysis; plant protection; veterinary medicine;
KW   human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia;
KW   screening; PCR primer; detection; probe; ss.
XX
OS   Synthetic.
XX
PN   DE19748690-A1.
XX
PD   06-MAY-1999.
XX
PF   04-NOV-1997;   97DE-1048690.
XX
PR   04-NOV-1997;   97DE-1048690.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
DR   WPI; 1999-278780/24.
XX
PT   Detecting nucleic acid by generating short amplicons and probing
PT   e.g. for diagnosis, food and environmental analysis and plant
PT   protection
XX
PS   Example 1; Page 17; 22pp; German.
XX
CC   This invention describes a method for the detection of nucleic acid
CC   which comprises amplification and reaction of the amplicon with a probe.
CC   The method is used to detect nucleic acid e.g. for medical or forensic
CC   diagnosis, in food and environmental analysis, in plant protection and
CC   veterinary medicine, e.g. for detecting human immune deficiency virus,
CC   hepatitis B or C viruses, or Chlamydia, in blood screening. The method
CC   provides target-dependent, exponential amplification for highly specific
CC   and sensitive, reproducible and quantitative detection of one or more
CC   nucleic acids (single or double stranded). The design of primers and
CC   probes is sufficiently flexible to allow many nucleic acids to be
CC   detected in a standardized reaction format using partly the same primers
CC   and probes. Only small amplicons are produced (requiring short
CC   amplification cycles), there is no competition/displacement between the
CC   short counter-strand of the amplicon and the detection probe, and
CC   specificity is high because the relative proportion of the internal
CC   detection region is increased with respect to the total amplicon length,
CC   allowing better differentiation between (viral) subtypes. Also short
CC   amplicons are less likely to undergo non-specific hybridization, so
CC   background is low, and short RNA sequences are more stable, with reduced
CC   tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
CC   PCR primers and probes used in the method of the invention.
XX
SQ   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 ctcgcaagcaccctatcaggcagt 24


RESULT  12
AAC66753/c
ID   AAC66753 standard; DNA; 24 BP.
XX
AC   AAC66753;
XX
DT   16-FEB-2001  (first entry)
XX
DE   PCR primer #2 used for detecting Hepatitis C virus.
XX
KW   PCR primer; virus detection; HCV core protein; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200063444-A2.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-EP04175.
XX
PR   14-APR-1999;   99US-0129319.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Budkowska A,  Maillard P,  Nitkiewicz J,  Crainic R;
XX
DR   WPI; 2000-679609/66.
XX
PT   Directly detecting hepatitis C virus in serum of patients comprises use
PT   of primers corresponding to viral RNA encoding core protein, or
PT   monoclonal antibodies recognizing core protein or nucleocapsid protein
PT   of the virus -
XX
PS   Claim 1; Page 22; 22pp; English.
XX
CC   The present invention relates to a method for directly detecting
CC   hepatitis C virus (HCV) in fractionated or non-fractionated serum of a
CC   patient. The method comprises detecting virus with primers corresponding
CC   to viral RNA encoding core protein. The present sequence is one such
CC   primer of the present invention. The method allows visualisation of the
CC   presence of the HCV by a double sandwich test. HCV core protein has a
CC   number of important roles, including modulation of transcription from
CC   cellular promoters, suppression of the HBV gene expression, interaction
CC   with the cytoplasmic tail of lymphotoxin receptor, as well as an
CC   important role in viral replication.
XX
SQ   Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 21;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     24 CTCGCAAGCACCCTATCAGGCAGT 1


RESULT  13
AAH25404
ID   AAH25404 standard; DNA; 24 BP.
XX
AC   AAH25404;
XX
DT   22-AUG-2001  (first entry)
XX
```

DE PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-EP11459.
XX
PR 17-NOV-1999; 99EP-0122853.
PR 12-MAY-2000; 2000EP-0110165.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 2001-381247/40.
XX
PT Novel composition of magnetic glass particles for purification of DNA
PT or RNA in automated processes -
XX
PS Example 7; Page 95; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between
CC 5-500 nm. The composition is useful for the purification of nucleic
CC acids. The composition can be used to process large quantities of
CC nucleic acid samples, because it does not involve the particles being
CC centrifuged or the fluids being drawn through glass fiber filters.
CC PCR primers AAH25403-04 were used to amplify HCV DNA fragments. The
CC amplified fragment can be purified using the method of the invention.
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 1 ctcgcaagcaccctatcaggcagt 24

RESULT 14
AAQ37587
ID AAQ37587 standard; DNA; 26 BP.
XX
AC AAQ37587;
XX
DT 23-JUN-1993 (first entry)
XX
DE HCV conserved region downstream primer/probe KY145, position 276-301.
XX
KW Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW regulation; US; Japan; C9; ss.
XX
OS Synthetic.
XX
PN EP529493-A.
XX
PD 03-MAR-1993.
XX
PF 19-AUG-1992; 92EP-0114115.
XX
PR 27-AUG-1991; 91US-0751305.
PR 21-JUL-1992; 92US-0918844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Resnick RM, Young KKY;
XX
DR WPI; 1993-068572/09.
XX
PT Compsn. comprising oligo:nucleotide probe-primer - used for
PT detecting hepatitis C virus strains Japan, US and C9
XX
PS Claim 3; Page 8; 43pp; English.
XX
CC The sequences given in AAQ37569-96 are oligonucleotides which can be
CC used as primers or probes which hybridise to the conserved region at
CC the 5'-end of the hepatitis C virus (HCV) genome. HCV is a small
CC RNA virus containing a small, positive sense, molecule of RNA about
CC 10,000 nucleotides in length. the genome contains a single, long,
CC open reading frame believed to translated in to a single, large
CC polyprotein and subsequently processed. The open reading frame
CC begins at nucleotide 343 (using the numbering system from the
CC prototype virus) following an untranslated region (UTR) the 5'UTR
CC sequence is relatively conserved and may be important in viral
CC replication and regulation. The 5' end of the coding region is also
CC conserved. These primer/probes can be used to identify different HCV
CC isolates such as US, Japan and C9 (see also AAQ37597-601).
XX
SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 3 ctcgcaagcaccctatcaggcagt 26

RESULT 15
AAQ68061
ID AAQ68061 standard; DNA; 26 BP.
XX
AC AAQ68061;
XX
DT 19-DEC-1994 (first entry)
XX
DE Primer HcPr96 for HCV genotyping (universal).
XX
KW Hepatitis C virus; HCV; probe; genotyping; hybridisation;
KW non-A, non-B hepatitis; NANBH; amplification; primer;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN WO9412670-A.
XX
PD 09-JUN-1994.
XX
PF 26-NOV-1993; 93WO-EP03325.
XX
PR 27-NOV-1992; 92EP-0403222.
PR 31-AUG-1993; 93EP-0402129.
XX
PA (INNO-) INNOGENETICS NV SA.
XX
PI Maertens G, Rossau R, Stuyver L, Van Heuverswyn H;
XX
DR WPI; 1994-200296/24.
XX
PT Process for genotyping Hepatitis C virus (HCV) isolates -
PT utilises probes hybridising to HCV isolate domains
XX
PS Claim 13; Page 73; 96pp; English.
XX

```
CC   Genotyping HCV utilises probes hybridising to HCV isolate domains.
CC   HCV types 2, 3, 4, 5 or 6 and subtypes 1a, 1b, 2a, 2b, 3a, 3b,
CC   3c, 4a, 4b, 4c, 4d, 4e, 4f, 4g and 4h can be typed.
CC   The hybridisation step is pref. preceded by an amplification
CC   step (PCR) using universal primers given in AAQ68058-61.
XX
SQ   Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 15;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 ctcgcaagcaccctatcaggcagt 26


RESULT  16
AAT64901
ID   AAT64901 standard; DNA; 26 BP.
XX
AC   AAT64901;
XX
DT   12-MAR-1998  (first entry)
XX
DE   Hepatitis C virus (HCV) oligonucleotide KY145.
XX
KW   Hepatitis C virus; reverse transcription; probe; PCR primer;
KW   detection; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   EP787807-A2.
XX
PD   06-AUG-1997.
XX
PF   19-AUG-1992;   92EP-0065347.
XX
PR   21-JUL-1992;   92US-0918844.
PR   27-AUG-1991;   91US-0751305.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Resnick RM,  Young KKY;
XX
DR   WPI; 1997-387489/36.
XX
PT   Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT   nucleic acid - from many different strains without loss of
PT   specificity, allow single step reverse transcription and
PT   amplification
XX
PS   Claims 4 and 5; Page 8; 35pp; English.
XX
CC   This oligonucleotide KY145 can be used as a probe for detecting
CC   hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC   strain as well as HCV C9 prototype strain. This oligonucleotide can
CC   also be used as a primer for amplifying HCV nucleic acid. The sequence
CC   of this oligonucleotide is contained in a specific region of HCV genomic
CC   nucleic acid. The probe or the primer is preferably labelled. The probe
CC   is used to detect HCV nucleic acid, preferably after this has been
CC   amplified using the new primer in reverse transcription polymerase chain
CC   reaction (RT-PCR), for both diagnostic and epidemiological applications.
CC   The primer is effective for both reverse transcription and PCR,
CC   eliminating the need to open the reaction tube during the procedure.
CC   Amplification is effective (no need for a second round of PCR with nested
CC   primers) and provides high sensitivity.  The probe is directed to
CC   conserved regions and so can detect many different strains without loss
CC   of specificity.
XX
SQ   Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 18;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 ctcgcaagcaccctatcaggcagt 26


RESULT  17
AAZ57408
ID   AAZ57408 standard; DNA; 26 BP.
XX
AC   AAZ57408;
XX
DT   07-APR-2000  (first entry)
XX
DE   Hepatitis C virus PCR primer A5'-II SEQ ID NO:23.
XX
KW   Hepatitis C virus; RNA virus; replication; viral infection;
KW   PCR primer; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9967394-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP03380.
XX
PR   24-JUN-1998;   98JP-0177820.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Kohara M,  Kohara K,  Taira K,  Matsuzaki J,  Ohmori H;
XX
DR   WPI; 2000-106296/09.
XX
PT   Vectors expressing full-length gene of RNA viruses, useful in
PT   clarifying mechanisms of RNA viral replication, infection, and
PT   developing remedies and therapeutics -
XX
PS   Example 2; Page 21; 46pp; Japanese.
XX
CC   The present invention describes a vector comprising a cDNA encoding an
CC   RNA virus gene, constructed to ensure the exact and homogeneous
CC   transcription of both terminals of the RNA virus gene. Also described
CC   is a method for screening drugs for inhibiting the replication of RNA
CC   virus by using the RNA viral infection model animal, particularly one
CC   with hepatitis C viral infection. The vector is useful in clarifying
CC   the mechanism of RNA viral replication, onset of RNA viral infection,
CC   and developing remedies and therapeutics for RNA viral infections,
CC   particularly of a hepatitis C virus. The present sequence represents
CC   a PCR primer which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 21;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      3 ctcgcaagcaccctatcaggcagt 26


RESULT  18
AAQ71839
ID   AAQ71839 standard; DNA; 27 BP.
```

XX
AC AAQ71839;
XX
DT 25-MAR-1995 (first entry)
XX
DE PCR primer for hepatitis G virus.
XX
KW DNA primer; sense; polymerase chain reaction; hepatitis G virus;
KW diagnostic; ss.
XX
OS Synthetic.
XX
PN WO9418217-A.
XX
PD 18-AUG-1994.
XX
PF 03-FEB-1993; 93WO-US00928.
XX
PR 03-FEB-1993; 93AU-0036061.
PR 03-FEB-1993; 93WO-US00928.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Hatzakis AE, Kuhns MC, Tassopoulos NC, Troonen H;
XX
DR WPI; 1994-279671/34.
XX
PT Hepaitis G virus polypeptides, nucleic acids, antibodies and cell
PT cultures - used to detect the virus in a test sample and to
PT screen antiviral agents
XX
PS Disclosure; Page 60; 67pp; English.
XX
CC The sense primer is used with an antisense primer (AAQ71840)
CC in a reverse transcription-polymerase chain reaction assay for
CC hepatitis E virus. A DNA probe (AAQ71841) is used to detect the PCR
CC products generated by the 2 primers.
XX
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 3 ctcgcaagcaccctatcaggcagt 26

RESULT 19
AAA74624
ID AAA74624 standard; DNA; 27 BP.
XX
AC AAA74624;
XX
DT 08-JAN-2001 (first entry)
XX
DE HCV-specific amplification primer C287R27.
XX
KW Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
XX
OS Hepatitis C virus.
XX
PN EP1026262-A2.
XX
PD 09-AUG-2000.
XX
PF 01-FEB-2000; 2000EP-0300763.
XX
PR 03-FEB-1999; 99US-0118497.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Linnen JM, Gorman KM;
XX
DR WPI; 2000-507254/46.
XX
PT Detecting hepatitis C virus in biological sample involves amplifying
PT reverse transcribed products of virus RNA using amplification primers
PT whose sequences correspond to 5' or 3' non-coding region of the virus
PT RNA -
XX
PS Claim 30; Page 27; 28pp; English.
XX
CC The present sequence is an amplification primer used in a method for
CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV
CC RNA is reverse transcribed to generate cDNA. This is then amplified
CC using primers, including the present sequence, corresponding to the
CC 5' or 3' non-coding region of HCV. The method is useful for the
CC diagnosis of HCV infection in patients, in testing the efficacy of
CC anti-HCV therapeutic regimes, and in screening blood for HCV-infected
CC samples. The method provides an improved single-round, reverse
CC transcription/amplification assay which detects low copy levels of HCV
CC RNA. The primers and assay system are designed to allow the
CC co-amplification of multiple regions of the HCV genome, multiple viral
CC species, and an internal positive control (IPC) RNA (or DNA).
CC Simultaneous amplification/detection of multiple regions of the HCV
CC genome increases assay sensitivity and the co-amplification of an IPC
CC decreases the likelihood of false negative results because of PCR
CC inhibition.
XX
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 3 ctcgcaagcaccctatcaggcagt 26

RESULT 20
AAZ87367
ID AAZ87367 standard; cDNA; 27 BP.
XX
AC AAZ87367;
XX
DT 22-MAY-2000 (first entry)
XX
DE Hepatitis C virus 5'NCR RT-PCR primer NC4.
XX
KW Hepatitis C virus; HCV; in vitro culture; primary mammalian hepatocyte;
KW culture medium; replication; drug screening; antibody testing;
KW diagnosis; vaccine development; 5'NCR; reverse transcriptase-PCR;
KW RT-PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO9967362-A1.
XX
PD 29-DEC-1999.
XX
PF 23-JUN-1999; 99WO-EP04337.
XX
PR 24-JUN-1998; 98EP-0401554.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Rumin S, Inchauspe G, Trepo C, Gripon P;
XX
DR WPI; 2000-160580/14.
XX
PT Use of a culture medium comprising at least one mammalian plasma or

```
PT   sera and antioxidants and/or corticoids, for in vitro replication of
PT   hepatitis C virus in hepatocytes  -
XX
PS   Example 3; Page 18; 39pp; English.
XX
CC   The invention relates to a novel process and cell culture medium for in
CC   vitro replication of hepatitis C virus (HCV) in primary mammalian
CC   hepatocytes. The culture medium comprising one or more mammalian
CC   plasma or sera, a chemical or biological compound with an
CC   anti-oxidative property and/or a differentiating property, such as
CC   dimethyl sulphoxide (DMSO), retinoic acid, vitamin (e.g., vitamin E),
CC   or selenium, and/or at least one corticoid. The culture medium may be
CC   used in an in vitro HCV infection and culture system. This would allow
CC   the mechanisms of viral replication to be studied, and could also be
CC   used for in vitro screening of anti-HCV drugs; to test neutralising
CC   antibodies; for in vitro diagnosis of HCV; and for the preparation of
CC   vaccines against HCV. The HCV-infected hepatocytes survive for at least
CC   4 months in the culture medium. Previously, a reliable and robust in
CC   vitro HCV culture method has not been available. Sequences
CC   AAZ87367-Z87375 represent reverse transcriptase-PCR (RT-PCR) primers used
CC   in an exemplification of the present invention.
XX
SQ   Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 21;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      2 ctcgcaagcaccctatcaggcagt 25


RESULT  21
ABA02736
ID   ABA02736 standard; RNA; 27 BP.
XX
AC   ABA02736;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Nucleic acid sensor molecule SEQ ID NO 8.
XX
KW   Nucleic acid sensor molecule; detection; infection; disease diagnosis;
KW   physiological abnormality; electronic; signalling molecule;
KW   nucleoside analogue; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..27
FT                   /*tag=  a
FT                   /mod_base= "OTHER"
FT                   /note= "2'-O-methyl nucleotides"
XX
PN   WO200166721-A2.
XX
PD   13-SEP-2001.
XX
PF   06-MAR-2001; 2001WO-US07163.
XX
PR   06-MAR-2000; 2000US-187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Usman N,  McSwiggen JA,  Zinnen S,  Seiwert S,  Haeberli P;
PI   Chowrira B,  Blatt L;
XX
DR   WPI; 2001-616242/71.
XX
PT   New nucleic acid sensor molecule useful in diagnostic applications,
PT   nucleic acid-based electronics and functional genomics, comprises an
PT   enzymatic nucleic acid and one or more sensors  -
XX
PS   Example 1; Page 69; 115pp; English.
XX
CC   The invention relates to a nucleic acid sensor molecule (I) comprising an
CC   enzymatic nucleic acid component and one or more sensor components. (I)
CC   is useful in diagnostic applications to identify the presence of genes
CC   and/or gene products indicative of a particular genotype and/or
CC   phenotype, e.g. a disease state or infection and for diagnosis of disease
CC   states or physiological abnormalities related to the expression of viral,
CC   bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based
CC   electronics, for the detection of specific target signalling molecules,
CC   in assays to assess the specificity, toxicity and effectiveness of
CC   various small molecules, nucleoside analogues or non-nucleic acid drugs
CC   or for detection of pathogens, biochemicals, organic or inorganic
CC   compounds. The present sequence is that of a nucleic acid sensor molecule
CC   of the invention.
XX
SQ   Sequence 27 BP; 8 A; 10 C; 5 G; 4 U; 0 other;


  Query Match             100.0%;  Score 24;  DB 22;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 4.4e-05;
  Matches   20;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          |:|||||||||||:|:|||||||:
Db      3 cucgcaagcacccuaucaggcagu 26


RESULT  22
ABA02738/c
ID   ABA02738 standard; RNA; 27 BP.
XX
AC   ABA02738;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Nucleic acid sensor molecule SEQ ID NO 10.
XX
KW   Nucleic acid sensor molecule; detection; infection; disease diagnosis;
KW   physiological abnormality; electronic; signalling molecule;
KW   nucleoside analogue; ss.
XX
OS   Synthetic.
XX
PN   WO200166721-A2.
XX
PD   13-SEP-2001.
XX
PF   06-MAR-2001; 2001WO-US07163.
XX
PR   06-MAR-2000; 2000US-187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Usman N,  McSwiggen JA,  Zinnen S,  Seiwert S,  Haeberli P;
PI   Chowrira B,  Blatt L;
XX
DR   WPI; 2001-616242/71.
XX
PT   New nucleic acid sensor molecule useful in diagnostic applications,
PT   nucleic acid-based electronics and functional genomics, comprises an
PT   enzymatic nucleic acid and one or more sensors  -
XX
PS   Example 1; Page 69; 115pp; English.
XX
CC   The invention relates to a nucleic acid sensor molecule (I) comprising an
CC   enzymatic nucleic acid component and one or more sensor components. (I)
CC   is useful in diagnostic applications to identify the presence of genes
CC   and/or gene products indicative of a particular genotype and/or
CC   phenotype, e.g. a disease state or infection and for diagnosis of disease
CC   states or physiological abnormalities related to the expression of viral,
```

CC bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based
CC electronics, for the detection of specific target signalling molecules,
CC in assays to assess the specificity, toxicity and effectiveness of
CC various small molecules, nucleoside analogues or non-nucleic acid drugs
CC or for detection of pathogens, biochemicals, organic or inorganic
CC compounds. The present sequence is that of a nucleic acid sensor molecule
CC of the invention.
XX
SQ Sequence 27 BP; 4 A; 5 C; 10 G; 8 U; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 25 CTCGCAAGCACCCTATCAGGCAGT 2

RESULT 23
AAH78439
ID AAH78439 standard; DNA; 27 BP.
XX
AC AAH78439;
XX
DT 10-DEC-2001 (first entry)
XX
DE PCR primer used to amplify HCV cDNA fragment.
XX
KW Protein isolation; magnetic colloidal particle; polymer envelope;
KW vaccine; HCV; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200152612-A2.
XX
PD 26-JUL-2001.
XX
PF 22-JAN-2001; 2001WO-FR00205.
XX
PR 21-JAN-2000; 2000FR-0000862.
XX
PA (INMR) BIO MERIEUX.
XX
PI Elaissari A, Mandrand B, Delair T, Spencer D, Arkis A;
XX
DR WPI; 2001-596423/67.
XX
PT Isolation of protein and protein-nucleic acid complexes, useful e.g.
PT for subsequent analysis or transport, by binding to magnetic beads
PT coated with functionalized polymer -
XX
PS Example 4; Page 13; 29pp; French.
XX
CC The specification describes a method for the isolation of proteins
CC and/or their complexes with nucleic acid. The method comprises treating
CC a sample with magnetic colloidal particles that comprise a magnetic
CC core and an envelope of a polymer (P1) containing ionizable functional
CC groups. The mixture is incubated then the proteins or complexes are
CC recovered by application of a magnetic field. The core is covered by
CC at least one polymer (P2) containing functional groups, at least some
CC of which have reacted with groups in (P1). Functional groups in P1
CC and P2 are the same or different, and are amino, hydroxy thiol, formyl,
CC ester, anhydride, acyl chloride, carbonate, carbamate and/or
CC iso(thio)cyanate. The method is used for extraction, identification,
CC detection and/or quantification of protein and their complexes. It is
CC also used for establishing cell cultures and biological samples. The
CC complexes formed between magnetic colloidal particles and the proteins
CC are useful for transfer, transport and/or storage of infectious agents
CC (virus, bacterium or yeast) and for preparation of vaccines. PCR
CC primers AAH78438-39 were used to amplify a fragment of HCV cDNA. The
CC amplified fragment was used to demonstrate the use of the method of the
CC invention for capture of HCV particles by magnetic latex.
XX
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 2 ctcgcaagcaccctatcaggcagt 25

RESULT 24
AAH78441
ID AAH78441 standard; DNA; 27 BP.
XX
AC AAH78441;
XX
DT 10-DEC-2001 (first entry)
XX
DE PCR primer used to amplify HCV cDNA fragment.
XX
KW Protein isolation; magnetic colloidal particle; polymer envelope;
KW vaccine; HCV; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200152612-A2.
XX
PD 26-JUL-2001.
XX
PF 22-JAN-2001; 2001WO-FR00205.
XX
PR 21-JAN-2000; 2000FR-0000862.
XX
PA (INMR) BIO MERIEUX.
XX
PI Elaissari A, Mandrand B, Delair T, Spencer D, Arkis A;
XX
DR WPI; 2001-596423/67.
XX
PT Isolation of protein and protein-nucleic acid complexes, useful e.g.
PT for subsequent analysis or transport, by binding to magnetic beads
PT coated with functionalized polymer -
XX
PS Example 4; Page 13; 29pp; French.
XX
CC The specification describes a method for the isolation of proteins
CC and/or their complexes with nucleic acid. The method comprises treating
CC a sample with magnetic colloidal particles that comprise a magnetic
CC core and an envelope of a polymer (P1) containing ionizable functional
CC groups. The mixture is incubated then the proteins or complexes are
CC recovered by application of a magnetic field. The core is covered by
CC at least one polymer (P2) containing functional groups, at least some
CC of which have reacted with groups in (P1). Functional groups in P1
CC and P2 are the same or different, and are amino, hydroxy thiol, formyl,
CC ester, anhydride, acyl chloride, carbonate, carbamate and/or
CC iso(thio)cyanate. The method is used for extraction, identification,
CC detection and/or quantification of protein and their complexes. It is
CC also used for establishing cell cultures and biological samples. The
CC complexes formed between magnetic colloidal particles and the proteins
CC are useful for transfer, transport and/or storage of infectious agents
CC (virus, bacterium or yeast) and for preparation of vaccines. PCR
CC primers AAH78440-41 were used to amplify a fragment of HCV cDNA. The
CC amplified fragment was used to demonstrate the use of the method of the
CC invention for capture of HCV particles by magnetic latex.
XX
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 27;

```
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db       2 ctcgcaagcaccctatcaggcagt 25


RESULT  25
ABK09262
ID   ABK09262 standard; RNA; 27 BP.
XX
AC   ABK09262;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Enzymatic nucleic acid effector molecule sequence I-2.3.
XX
KW   Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW   cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW   muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW   DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW   B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW   human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW   MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW   inflammatory arthropathy; central nervous system injury;
KW   cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW   chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW   Parkinson's disease; ataxia; Huntington's disease;
KW   Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200159103-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04273.
XX
PR   11-FEB-2000; 2000US-181797P.
PR   28-FEB-2000; 2000US-185516P.
PR   06-MAR-2000; 2000US-187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
PA   (CHOW/) CHOWRIRA B M.
XX
PI   Blatt L,  McSwiggen J,  Chowrira BM;
XX
DR   WPI; 2001-607195/69.
XX
PT   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT   constructs, which down regulate expression of a CD20 gene or neurite
PT   growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
PT   and central nervous system injury  -
XX
PS   Example 7; Page 170; 200pp; English.
XX
CC   The invention relates to a nucleic acid molecule which down regulates
CC   expression of a CD20 gene and a nucleic acid molecule which down
CC   regulates expression of a neurite growth inhibitor gene (NOGO).
CC   The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC   DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC   possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
CC   motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme
CC   (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
CC   to cleave RNA of CD20 in the presence of a divalent cation that is
CC   preferably Mg^2^+. Furthermore, it may be contacted with a cell to reduce
CC   CD20 activity of the cell and treat a patient having a condition
CC   associated with the level of CD20. The treatment may further comprise the
CC   use of one or more therapies. In particular, the CD20 targetting
CC   nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC   lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC   low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC   immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC   immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC   thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting
CC   nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
CC   divalent cation that is preferably Mg^2^+. Furthermore, the nucleic acid
CC   may be contacted with a cell to reduce NOGO activity of the cell and
CC   treat a patient having a condition associated with the level of NOGO. The
CC   treatment may further comprise the use of one or more therapies.
CC   In particular, the NOGO-targetting nucleic acid may be used to treat
CC   central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC   stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC   chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC   Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC   disease, muscular dystrophy, and/or other neurodegenerative disease
CC   states which respond to the modulation of NOGO expression. The
CC   present sequence is an enzymatic nucleic acid with trans-acting
CC   inhibitory sequences (S- are substrate sequences, Rz-  are enzymatic
CC   nucleic acid and I- are inhibitory sequences).
XX
SQ   Sequence 27 BP; 8 A; 10 C; 5 G; 4 U; 0 other;


  Query Match             100.0%;  Score 24;  DB 23;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 4.4e-05;
  Matches   20;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           |:|||||||||||:|:|||||||:
Db       3 cucgcaagcacccuaucaggcagu 26


RESULT  26
ABK09264/c
ID   ABK09264 standard; RNA; 27 BP.
XX
AC   ABK09264;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Enzymatic nucleic acid effector molecule sequence I-2.5.
XX
KW   Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW   cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW   muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW   DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW   B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW   human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW   MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW   inflammatory arthropathy; central nervous system injury;
KW   cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW   chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW   Parkinson's disease; ataxia; Huntington's disease;
KW   Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200159103-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04273.
XX
PR   11-FEB-2000; 2000US-181797P.
PR   28-FEB-2000; 2000US-185516P.
PR   06-MAR-2000; 2000US-187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
```

PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, McSwiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
PT and central nervous system injury -
XX
PS Example 7; Page 170; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO).
CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
CC motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme
CC (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
CC to cleave RNA of CD20 in the presence of a divalent cation that is
CC preferably Mg^2^+. Furthermore, it may be contacted with a cell to reduce
CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targetting
CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting
CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
CC divalent cation that is preferably Mg^2^+. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NOGO activity of the cell and
CC treat a patient having a condition associated with the level of NOGO. The
CC treatment may further comprise the use of one or more therapies.
CC In particular, the NOGO-targetting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The
CC present sequence is an enzymatic nucleic acid with trans-acting
CC inhibitory sequences (S- are substrate sequences, Rz- are enzymatic
CC nucleic acid and I- are inhibitory sequences).
XX
SQ Sequence 27 BP; 4 A; 5 C; 10 G; 8 U; 0 other;

Query Match 100.0%; Score 24; DB 23; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 25 CTCGCAAGCACCCTATCAGGCAGT 2

RESULT 27
AAT05222
ID AAT05222 standard; DNA; 28 BP.
XX
AC AAT05222;
XX
DT 13-JUN-1996 (first entry)
XX
DE Hepatitis C virus antisense oligonucleotide A312.
XX
KW Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
KW infection; antisense; non coding; region; NCR; core region; ss.
XX
OS Synthetic.
XX
PN WO9530746-A1.
XX
PD 16-NOV-1995.
XX
PF 08-MAY-1995; 95WO-US05812.
XX
PR 10-MAY-1994; 94US-0240382.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Wakita T, Wands JR;
XX
DR WPI; 1995-404113/51.
XX
PT New anti:sense hepatitis C virus oligo:nucleotide(s) - used for
PT inhibiting HCV RNA translation, for the treatment or prevention of
PT HCV infection
XX
PS Claim 1; Page 29; 50pp; English.
XX
CC The present oligonucleotide (ON) inhibits the expression of
CC hepatitis C virus (HCV) RNA, specifically HCV type II and type III
CC protein synthesis is inhibited by 45% and 18%, respectively. The
CC ONs of the invention inhibit translation of HCV types I-V RNA in
CC vivo, ex vivo or in vitro, and can therefore be used to treat or
CC prevent HCV infection. The antisense ONs comprise 10-28
CC nucleotides complementary to the entire HCV 5'-non-coding and part
CC of the core region. The A or S in the ONs name denotes antisense
CC or sense, and the no. indicates the position of the 5'-end of the
CC ON. The ON was tested at 10 fold molar excess to HCV RNA.
XX
SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 2 ctcgcaagcaccctatcaggcagt 25

RESULT 28
AAZ57757
ID AAZ57757 standard; DNA; 28 BP.
XX
AC AAZ57757;
XX
DT 05-APR-2000 (first entry)
XX
DE Hepatitis C virus antisense inhibitor oligonucleotide A312.
XX
KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
KW anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
OS Hepatitis C virus.
XX
PN US6001990-A.
XX
PD 14-DEC-1999.
XX
PF 07-JUN-1995; 95US-0474700.
XX
PR 10-MAY-1994; 94US-0240382.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Moradpour D, Wands JR, Wakita T;
XX

DR WPI; 2000-104900/09.
XX
PT Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
PT Hepatitis C virus infections -
XX
PS Claim 1; Column 23; 31pp; English.
XX
CC This sequence is an antisense oligonucleotide that hybridises to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma.
XX
SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 2 ctcgcaagcaccctatcaggcagt 25

RESULT 29
AAQ55728
ID AAQ55728 standard; DNA; 30 BP.
XX
AC AAQ55728;
XX
DT 13-OCT-1994 (first entry)
XX
DE Hepatitis C detection primer 2.
XX
KW Key.
XX
OS Synthetic.
XX
PN JP06014800-A.
XX
PD 25-JAN-1994.
XX
PF 02-JUL-1992; 92JP-0197407.
XX
PR 02-JUL-1992; 92JP-0197407.
XX
PA (TOYJ) TOSOH CORP.
XX
DR WPI; 1994-061488/08.
XX
PT Detection of human hepatitic C virus - using primer contg. at
PT least 15 continuous bases
XX
PS Claim 1; Page 1; 5pp; Japanese.
XX
CC The primers (AAQ55727-728) are used to detect hepatitis C virus.
CC The method can amplify and detect specifically the nucleic acid
CC sequence originated from a trace amount of HCV contained in a
CC sample.
XX
SQ Sequence 30 BP; 8 A; 12 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 4 ctcgcaagcaccctatcaggcagt 27

RESULT 30
AAQ31158
ID AAQ31158 standard; DNA; 33 BP.
XX
AC AAQ31158;
XX
DT 24-MAR-1993 (first entry)
XX
DE Probe 127 for genotyping analysis of HCV-1.
XX
KW Hepatitis C virus; non-A, non-B hepatitis; polymerase chain reaction;
KW amplified solution phase nucleic acid sandwich assay;
KW genotyping analysis; capture probe; detection probe; ss.
XX
OS Synthetic.
XX
PN WO9219743-A.
XX
PD 12-NOV-1992.
XX
PF 08-MAY-1992; 92WO-US04036.
XX
PR 08-MAY-1991; 91US-0697326.
XX
PA (CHIR) CHIRON CORP.
XX
PI Beall E, Cha T, Irvine B, Kolberg J, Urdea MS;
XX
DR WPI; 1992-398869/48.
XX
PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence
PT - related to HCV-1, useful for treating and detecting HCV-1
PT infections and as a vaccine
XX
PS Claim 63; Page 140; 186pp; English.
XX
CC A sandwich hybridisation assay can be used for HCV-1 genotyping
CC analysis. One example uses nucleotide sequences which correspond to
CC sequences in the C gene and the 5' UT region of HCV isolates as either
CC capture or detection probes. Probe 127 is preferably used as a capture
CC probe.
XX
SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 13; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgcaagcaccctatcaggcagt 24
||||||||||||||||||||||||
Db 7 ctcgcaagcaccctatcaggcagt 30

RESULT 31
AAQ46464
ID AAQ46464 standard; DNA; 33 BP.
XX
AC AAQ46464;
XX
DT 13-DEC-1993 (first entry)
XX
DE Hepatitis C virus RNA assay capture probe HCV.33.9.
XX
KW Detection; HCV; reduced background signal; improved reproducibility;
KW hybridisation; 5'-untranslated region; C gene; ss.
XX
OS Synthetic.

```
XX
PN   WO9313224-A.
XX
PD   08-JUL-1993.
XX
PF   22-DEC-1992;   92WO-US11343.
XX
PR   23-DEC-1991;   91US-0813338.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Chang C,  Running J,  Sheridan P;
XX
DR   WPI; 1993-227338/28.
XX
PT   Immobilising nucleic acid probe on styrene, useful for HCV
PT   sequence detection - by using intermediate passively adsorbed
PT   polymer having functional gps. for covalently bonding to probe
PT   via its base-stable linkages
XX
PS   Example; Fig 3.1; 34pp; English.
XX
CC   The sequence is that of a synthetic capture probe which is
CC   complementary to nucleotide sequences in the hepatitis C virus
CC   C gene and the 5'-untranslated region. It may be used in an
CC   assay for the detection of HCV RNA.
XX
SQ   Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 14;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 ctcgcaagcaccctatcaggcagt 30


RESULT  32
AAV07838
ID   AAV07838 standard; DNA; 33 BP.
XX
AC   AAV07838;
XX
DT   10-DEC-1998  (first entry)
XX
DE   HCV.33.9 amplifier probe.
XX
KW   Comb-type branched polynucleotide; amplification multimer; analyte;
KW   hybridisation assay; hepatitis c virus; HCV; amplifier probe; ss.
XX
OS   Synthetic.
OS   Hepatitis c virus.
XX
PN   US5710264-A.
XX
PD   20-JAN-1998.
XX
PF   07-JUN-1995;   90US-0478085.
XX
PR   23-DEC-1991;   91US-0813588.
PR   27-JUL-1990;   90US-0558897.
PR   07-JUN-1995;   95US-0478085.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Chang C,  Fultz TJ,  Horn T,  Urdea MS,  Warner B;
XX
DR   WPI; 1998-109872/10.
XX
PT   New large comb-type branched polynucleotides - useful as
PT   amplification multimers in nucleic acid hybridisation assays
XX
PS   Example 6; Column 25; 33pp; English.
XX
CC   The invention relates to a large comb-type branched polynucleotide
CC   of formula: 3'-A-S-(S'-X')m-S''-5'; where X' is a branched site joined
CC   to  -(R)n-S'''-E-L; A = an oligonucleotide complementary to an analyte
CC   nucleic acid sequence; S = a first spacer segment of 1-50 linked monomers
CC   where each monomer is selected from nucleotides and a cleavable linker
CC   R; S' = a branching site spacer segment of 0-15 linked monomers where
CC   each of the monomers is selected from nucleotides and cleavable linker R;
CC   X' = a multifunctional nucleotide that provides a branch site; m = 1-100;
CC   S'' = a second spacer segment of 0-10 linked monomers where each of the
CC   monomers is selected from nucleotides and cleavable linker R; R = a
CC   cleavable linker molecule; n = 0 or 1; S''' = a third spacer segment of
CC   0-10 linked monomers where each of the monomers is selected from
CC   nucleotides and cleavable linker R; E = an oligonucleotide segment of 5-
CC   10 nucleotides; L = an oligonucleotide containing 2-10 iterations of a
CC   nucleotide sequence complementary to a labelled nucleic acid probe.
CC   The invention also relates to a branched nucleic acid polymer. The poly-
CC   nucleotides are useful as amplification multimers in nucleic acid
CC   hybridisation assays used for genetic research, biomedical research and
CC   clinical diagnostics. Since the polynucleotide multimers include a large
CC   number (at least 20) iterations of a sequence that are available for
CC   specific hybridisation, they permit a greater degree of amplification
CC   and decrease the threshold level of a detectable analyte. The present
CC   sequence represents a hepatitis c virus (HCV) amplifier probe.
XX
SQ   Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 19;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 ctcgcaagcaccctatcaggcagt 30


RESULT  33
AAV83066
ID   AAV83066 standard; DNA; 33 BP.
XX
AC   AAV83066;
XX
DT   24-FEB-1999  (first entry)
XX
DE   Amplifier probe HCV.33.9.
XX
KW   Comb-type branched polynucleotide; amplifier probe;
KW   multifunctional nucleotide; pendant polynucleotide sidechain;
KW   hybridisation assay; amplification multimer; sandwich assay; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   US5849481-A.
XX
PD   15-DEC-1998.
XX
PF   05-JUN-1995;   95US-0470124.
XX
PR   23-DEC-1991;   91US-0813588.
PR   27-JUL-1990;   90US-0558897.
PR   05-JUN-1995;   95US-0470124.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Chang C,  Fultz TJ,  Horn T,  Urdea MS,  Warner B;
XX
DR   WPI; 1999-069715/06.
XX
PT   Improved nucleic acid hybridisation assays - using large comb-type
```

```
PT   polypeptide(s)
XX
PS   Example 6; Column 24; 31pp; English.
XX
CC   Oligonucleotides AAV83063-80 represent amplifier probes, used in a
CC   sandwich hybridisation assay for Hepatitis C virus (HCV) DNA. The
CC   sandwich hybridisation assay utilises the comb-type branched
CC   polynucleotide amplification multimer of the invention. This large
CC   comb-type branched polynucleotide comprises a polynucleotide
CC   backbone having at least 15 multifunctional nucleotides each defining a
CC   sidechain site and pendant polynucleotide sidechains extending from the
CC   multifunctional nucleotides, each comprising iterations of an single
CC   stranded oligonucleotide unit capable of binding specifically to a
CC   second single-stranded polynucleotide sequence. The total number of
CC   iterations in all sidechains is at least 20. The first single-stranded
CC   polynucleotide sequence is a labelled polynucleotide, directly or
CC   indirectly linked to a nucleic acid analyte. In the nucleic acid
CC   hybridisation assay of the invention, the labelled nucleic acid probe
CC   is hybridised to the branched polymeric nucleotide via the second
CC   single-stranded oligonucleotide unit. The comb-type branched
CC   polynucleotides are used as amplification multimers in nucleic acid
CC   hybridisation assays and other assays such as direct, indirect and
CC   sandwich assays.
XX
SQ   Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 20;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db       7 ctcgcaagcaccctatcaggcagt 30


RESULT  34
AAV54436
ID   AAV54436 standard; DNA; 40 BP.
XX
AC   AAV54436;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence of HCV PCR primer 3.
XX
KW   Hepatitis C virus; HCV; PCR; primer; amplification; ss.
XX
OS   Synthetic.
XX
PN   JP10248579-A.
XX
PD   22-SEP-1998.
XX
PF   05-MAR-1997;   97JP-0067321.
XX
PR   05-MAR-1997;   97JP-0067321.
XX
PA   (SRLS-) SRL KK.
PA   (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
XX
DR   WPI; 1998-560731/48.
XX
PT   Determination of hepatitis C virus (HCV) gene - with real time
PT   detective PCR and primer and probe used for determination
XX
PS   Claim 3; Page 6; 7pp; Japanese.
XX
CC   This is the nucleotide sequence of a Hepatitis C virus (HCV) PCR primer
CC   used for amplification in the method of the invention.  This is a useful
CC   for the detection of the HCV gene.
XX
SQ   Sequence 40 BP; 9 A; 17 C; 9 G; 5 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 19;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db      13 ctcgcaagcaccctatcaggcagt 36


RESULT  35
AAQ98139
ID   AAQ98139 standard; DNA; 53 BP.
XX
AC   AAQ98139;
XX
DT   05-FEB-1996  (first entry)
XX
DE   Control label extender probe used in an HCV sandwich hybridisation assay.
XX
KW   Probe; nucleotide; solution phase sandwich hybridisation assay;
KW   competitive; analyte binding sequence; background signal reduction;
KW   comb body; Hepatitis C virus; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    21..53
FT                   /*tag=  a
FT                   /note= "hybridises to target sequence"
XX
PN   WO9516055-A1.
XX
PD   15-JUN-1995.
XX
PF   07-DEC-1994;   94WO-US14119.
XX
PR   08-DEC-1993;   93US-0164388.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Collins M,  Fultz T,  Urdea MS,  Warner BD;
XX
DR   WPI; 1995-224335/29.
XX
PT   Soln. phase sandwich hybridisation assays for nucleic acid(s) - with
PT   capture extender molecules or competitive oligo:nucleotide(s) to
PT   minimise background signal, increasing sensitivity and selectivity
XX
PS   Example 2; Page 43; 86pp; English.
XX
CC   AAQ98125-Q98143 are control label extender probes (LEs) used in a
CC   hepatitis C virus sandwich hybrisation assay used to demonstrate a
CC   variation of a new improved method of a solution phase sandwich
CC   hybridisation assay in which LEs are used with a capture probe (CP).
CC   One label extender probe binds the target DNA and another binds to a
CC   labelledprobe (LP).
CC   The new method minimises background signals (caused by non-specific
CC   hybridisation), this improves both sensitivity and selectivity of
CC   the assay without increasing cost or time.
XX
SQ   Sequence 53 BP; 12 A; 17 C; 15 G; 9 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 16;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db      27 ctcgcaagcaccctatcaggcagt 50
```

```
RESULT  36
AAQ98104
ID   AAQ98104 standard; DNA; 53 BP.
XX
AC   AAQ98104;
XX
DT   05-FEB-1996  (first entry)
XX
DE   Label extender probe used in an improved sandwich hybridisation assay.
XX
KW   Probe; nucleotide; solution phase sandwich hybridisation assay;
KW   competitive; analyte binding sequence; background signal reduction;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9516055-A1.
XX
PD   15-JUN-1995.
XX
PF   07-DEC-1994;   94WO-US14119.
XX
PR   08-DEC-1993;   93US-0164388.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Collins M,  Fultz T,  Urdea MS,  Warner BD;
XX
DR   WPI; 1995-224335/29.
XX
PT   Soln. phase sandwich hybridisation assays for nucleic acid(s) - with
PT   capture extender molecules or competitive oligo:nucleotide(s) to
PT   minimise background signal, increasing sensitivity and selectivity
XX
PS   Example 1; Page 33; 86pp; English.
XX
CC   AAQ98100-Q98105 are label extender probes (LEs) used in a variation
CC   of a new improved method of a solution phase sandwich hybridisation
CC   assay in which LEs are used with a capture probe (CP). One label
CC   extender probe binds the target DNA and another binds to a labelled
CC   probe (LP).
CC   The new method minimises background signals (caused by non-specific
CC   hybridisation), this improves both sensitivity and selectivity of
CC   the assay without increasing cost or time.
XX
SQ   Sequence 53 BP; 12 A; 17 C; 15 G; 9 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 16;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     27 ctcgcaagcaccctatcaggcagt 50


RESULT  37
AAQ63223/c
ID   AAQ63223 standard; RNA; 57 BP.
XX
AC   AAQ63223;
XX
DT   13-JUN-1994  (first entry)
XX
DE   Hepatitis C virus probe target region.
XX
KW   Detection; HCV; 11:2 probe design.
XX
OS   Hepatitis C virus.
XX
PN   WO9324656-A.
XX
PD   09-DEC-1993.
XX
PF   24-MAY-1993;   93WO-US04863.
XX
PR   29-MAY-1992;   92US-0891543.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Carrino JJ,  Marshall RL,  Sustachek JC;
XX
DR   WPI; 1993-405844/50.
XX
PT   Amplifying known RNA target for use in diagnosis of HIV and HCV
PT   infection - by treating sample RNA with oligo-nucleotide probe,
PT   extending probe by reverse transcription of target, dissociating
PT   probe from target, hybridising 2nd probe with 1st, etc.
XX
PS   Example 8; Page 26; 49pp; English.
XX
CC   The sequence is that of the target region of probes (AAQ53257-Q53260)
CC   used in the detection of hepatitis C virus (HCV) using a 11:2 probe
CC   design. It corresponds to positions 246-302 of the 5' UTR of the
CC   HPCHUMR sequence.
XX
SQ   Sequence 57 BP; 9 A; 9 C; 23 G; 16 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 14;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     57 CTCGCAAGCACCCTATCAGGCAGT 34


RESULT  38
AAZ23543/c
ID   AAZ23543 standard; DNA; 59 BP.
XX
AC   AAZ23543;
XX
DT   21-DEC-1999  (first entry)
XX
DE   HCV DNA fragment 2.
XX
KW   Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW   cellular; yeast; fungal; primer; ss.
XX
OS   Hepatitis C virus.
XX
PN   DE19814828-A1.
XX
PD   07-OCT-1999.
XX
PF   02-APR-1998;   98DE-1014828.
XX
PR   02-APR-1998;   98DE-1014828.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Kessler C,  Haberhausen G,  Batz H,  Oerum H;
XX
DR   WPI; 1999-552286/47.
XX
PT   Nucleic acid amplification assay for detecting viral, bacterial,
PT   cellular, yeast or fungal nucleic acids  -
XX
PS   Disclosure; Fig 7; 28pp; German.
XX
CC   This invention describes a novel assay for a nucleic acid comprises:
CC   (a) generating amplification products from a fragment of the nucleic
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CC   acid, (b) contacting the amplification products with a probe; and
CC   (c) detecting hybridization between the amplification product and the
CC   probe. The assay is useful for detection of viral, bacterial, cellular,
CC   yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
CC   or fungal samples, e.g. feces, smears, cell suspensions, cultures or
CC   tissue, cell or liquid biopsy samples. This sequence represents a
CC   fragment of the HCV genome used in the method of the invention.
XX
SQ   Sequence 59 BP; 9 A; 16 C; 21 G; 13 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 20;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db      26 CTCGCAAGCACCCTATCAGGCAGT 3


RESULT  39
AAZ09795/c
ID   AAZ09795 standard; DNA; 59 BP.
XX
AC   AAZ09795;
XX
DT   26-NOV-1999  (first entry)
XX
DE   HCV DNA probe.
XX
KW   Probe; amplification; primer; reporter group; quencher group; PCR;
KW   amplicon; detection; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   DE19814001-A1.
XX
PD   30-SEP-1999.
XX
PF   28-MAR-1998;   98DE-1014001.
XX
PR   28-MAR-1998;   98DE-1014001.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Kessler C,  Haberhausen G,  Batz H,  Orum H;
XX
DR   WPI; 1999-552213/47.
XX
PT   Fluorescent nucleic acid amplification assay, useful for detection of
PT   viral, bacterial, cellular, yeast or fungal nucleic acids -
XX
PS   Disclosure; Fig 4; 16pp; German.
XX
CC   This invention describes a novel assay for a nucleic acid which comprises
CC   an amplification reaction using two non-overlapping primers, a polymerase
CC   with 5'-nuclease activity and a probe with reporter groups and quencher
CC   groups that binds a region other than that bound by the primers. The
CC   reaction generates products of less than 100 nucleotides. The assay is
CC   useful for detection of viral, bacterial, cellular, yeast or fungal
CC   nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC   samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC   or liquid biopsy samples. Compared with assays in which longer
CC   amplification products are generated, the assay can be performed more
CC   rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
CC   may be increased due to reduced competition between the short
CC   counterstrand of the amplicon and the detector probe. Specificity may
CC   also be increased because of the increased relative length of sequence B
CC   compared with the total length of the amplicon and the differentiability
CC   of subtypes may be increased. In addition signal-to-noise ratios may be
CC   increased with the new method because short amplicons have reduced
CC   potential for nonspecific hybridization. In addition reproducibility may
CC   be increased because small target regions on RNA genomes are less
CC   sensitive to RNA degradation, and the possibilities for secondary
CC   structure formation are reduced. This sequence represents a probe used to
CC   detect hepatitis C virus which is used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 59 BP; 9 A; 16 C; 21 G; 13 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 20;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctcgcaagcaccctatcaggcagt 24
           ||||||||||||||||||||||||
Db      26 CTCGCAAGCACCCTATCAGGCAGT 3


RESULT  40
AAQ98121
ID   AAQ98121 standard; DNA; 64 BP.
XX
AC   AAQ98121;
XX
DT   05-FEB-1996  (first entry)
XX
DE   Label extender probe used in an HCV sandwich hybridisation assay.
XX
KW   Probe; nucleotide; solution phase sandwich hybridisation assay;
KW   competitive; analyte binding sequence; background signal reduction;
KW   comb body; Hepatitis C virus; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    17..49
FT                   /*tag= a
FT                   /note= "hybridises to target sequence"
XX
PN   WO9516055-A1.
XX
PD   15-JUN-1995.
XX
PF   07-DEC-1994;   94WO-US14119.
XX
PR   08-DEC-1993;   93US-0164388.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Collins M,  Fultz T,  Urdea MS,  Warner BD;
XX
DR   WPI; 1995-224335/29.
XX
PT   Soln. phase sandwich hybridisation assays for nucleic acid(s) - with
PT   capture extender molecules or competitive oligo:nucleotide(s) to
PT   minimise background signal, increasing sensitivity and selectivity
XX
PS   Example 2; Page 42; 86pp; English.
XX
CC   AAQ98118-Q98124 are label extender probes (LEs) used in a hepatitis C
CC   virus sandwich hybrisation assay used to demonstrate a variation
CC   of a new improved method of a solution phase sandwich hybridisation
CC   assay in which LEs are used with a capture probe (CP). One label
CC   extender probe binds the target DNA and another binds to a labelled
CC   probe (LP).
CC   The new method minimises background signals (caused by non-specific
CC   hybridisation), this improves both sensitivity and selectivity of
CC   the assay without increasing cost or time.
XX
SQ   Sequence 64 BP; 18 A; 16 C; 17 G; 13 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 16;  Length 64;
```

```
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db     23 ctcgcaagcaccctatcaggcagt 46


RESULT  41
AAQ53257
ID   AAQ53257 standard; DNA; 23 BP.
XX
AC   AAQ53257;
XX
DT   13-JUN-1994  (first entry)
XX
DE   Hepatitis C virus probe.
XX
KW   Detection; HCV; 11:2 probe design.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /note= "fluorescein labelled"
XX
PN   WO9324656-A.
XX
PD   09-DEC-1993.
XX
PF   24-MAY-1993;   93WO-US04863.
XX
PR   29-MAY-1992;   92US-0891543.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Carrino JJ,  Marshall RL,  Sustachek JC;
XX
DR   WPI; 1993-405844/50.
XX
PT   Amplifying known RNA target for use in diagnosis of HIV and HCV
PT   infection - by treating sample RNA with oligo-nucleotide probe,
PT   extending probe by reverse transcription of target, dissociating
PT   probe from target, hybridising 2nd probe with 1st, etc.
XX
PS   Example 8; Page 25; 49pp; English.
XX
CC   The sequence is that of a probe which was used in the detection of
CC   hepatitis C virus (HCV) using a 11:2 probe design. The probe is
CC   specific for a part of the 5' UTR of the HPCHUMR sequence between
CC   positions 246-302.
XX
SQ   Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 other;


  Query Match             95.8%;  Score 23;  DB 14;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.00017;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      1 tcgcaagcaccctatcaggcagt 23


RESULT  42
AAQ37588
ID   AAQ37588 standard; DNA; 29 BP.
XX
AC   AAQ37588;
XX
DT   23-JUN-1993  (first entry)
XX
DE   HCV conserved region downstream primer/probe KY95, position 276-298.
XX
KW   Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW   virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW   prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW   regulation; US; Japan; C9; ss.
XX
OS   Synthetic.
XX
PN   EP529493-A.
XX
PD   03-MAR-1993.
XX
PF   19-AUG-1992;   92EP-0114115.
XX
PR   27-AUG-1991;   91US-0751305.
PR   21-JUL-1992;   92US-0918844.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Resnick RM,  Young KKY;
XX
DR   WPI; 1993-068572/09.
XX
PT   Compsn. comprising oligo:nucleotide probe-primer - used for
PT   detecting hepatitis C virus strains Japan, US and C9
XX
PS   Claim 3; Page 8; 43pp; English.
XX
CC   The sequences given in AAQ37569-96 are oligonucleotides which can be
CC   used as primers or probes which hybridise to the conserved region at
CC   the 5'-end of the hepatitis C virus (HCV) genome.  HCV is a small
CC   RNA virus containing a small, positive sense, molecule of RNA about
CC   10,000 nucleotides in length.  the genome contains a single, long,
CC   open reading frame believed to translated in to a single, large
CC   polyprotein and subsequently processed.  The open reading frame
CC   begins at nucleotide 343 (using the numbering system from the
CC   prototype virus) following an untranslated region (UTR) the 5'UTR
CC   sequence is relatively conserved and may be important in viral
CC   replication and regulation.  The 5' end of the coding region is also
CC   conserved.  These primer/probes can be used to identify different HCV
CC   isolates such as US, Japan and C9 (see also AAQ37597-601).
XX
SQ   Sequence 29 BP; 8 A; 8 C; 8 G; 5 T; 0 other;


  Query Match             95.8%;  Score 23;  DB 14;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00017;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          ||||||||||||||||||||||||
Db      7 tcgcaagcaccctatcaggcagt 29


RESULT  43
AAT64902
ID   AAT64902 standard; DNA; 29 BP.
XX
AC   AAT64902;
XX
DT   12-MAR-1998  (first entry)
XX
DE   Hepatitis C virus (HCV) oligonucleotide KY95.
XX
KW   Hepatitis C virus; reverse transcription; probe; PCR primer;
KW   detection; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   EP787807-A2.
XX
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```
PD   06-AUG-1997.
XX
PF   19-AUG-1992;   92EP-0065347.
XX
PR   21-JUL-1992;   92US-0918844.
PR   27-AUG-1991;   91US-0751305.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Resnick RM,  Young KKY;
XX
DR   WPI; 1997-387489/36.
XX
PT   Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT   nucleic acid - from many different strains without loss of
PT   specificity, allow single step reverse transcription and
PT   amplification
XX
PS   Claims 4 and 5; Page 8; 35pp; English.
XX
CC   This oligonucleotide KY95 can be used as a probe for detecting
CC   hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC   strain as well as HCV C9 prototype strain. This oligonucleotide can
CC   also be used as a primer for amplifying HCV nucleic acid. The sequence
CC   of this oligonucleotide is contained in a specific region of HCV genomic
CC   nucleic acid. The probe or the primer is preferably labelled. The probe
CC   is used to detect HCV nucleic acid, preferably after this has been
CC   amplified using the new primer in reverse transcription polymerase chain
CC   reaction (RT-PCR), for both diagnostic and epidemiological applications.
CC   The primer is effective for both reverse transcription and PCR,
CC   eliminating the need to open the reaction tube during the procedure.
CC   Amplification is effective (no need for a second round of PCR with nested
CC   primers) and provides high sensitivity.  The probe is directed to
CC   conserved regions and so can detect many different strains without loss
CC   of specificity.
XX
SQ   Sequence 29 BP; 8 A; 8 C; 8 G; 5 T; 0 other;


  Query Match             95.8%;  Score 23;  DB 18;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00017;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tcgcaagcaccctatcaggcagt 24
          |||||||||||||||||||||||
Db      7 tcgcaagcaccctatcaggcagt 29


RESULT  44
AAQ53259/c
ID   AAQ53259 standard; DNA; 22 BP.
XX
AC   AAQ53259;
XX
DT   13-JUN-1994  (first entry)
XX
DE   Hepatitis C virus probe.
XX
KW   Detection; HCV; 11:2 probe design.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   22
FT                   /*tag=  a
FT                   /note= "fluorescein labelled"
XX
PN   WO9324656-A.
XX
PD   09-DEC-1993.
XX
PF   24-MAY-1993;   93WO-US04863.
XX
PR   29-MAY-1992;   92US-0891543.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Carrino JJ,  Marshall RL,  Sustachek JC;
XX
DR   WPI; 1993-405844/50.
XX
PT   Amplifying known RNA target for use in diagnosis of HIV and HCV
PT   infection - by treating sample RNA with oligo-nucleotide probe,
PT   extending probe by reverse transcription of target, dissociating
PT   probe from target, hybridising 2nd probe with 1st, etc.
XX
PS   Example 8; Page 25; 49pp; English.
XX
CC   The sequence is that of a probe which was used in the detection of
CC   hepatitis C virus (HCV) using a 11:2 probe design. The probe is
CC   specific for a part of the 5' UTR of the HPCHUMR sequence between
CC   positions 246-302.
XX
SQ   Sequence 22 BP; 3 A; 4 C; 9 G; 6 T; 0 other;


  Query Match             91.7%;  Score 22;  DB 14;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.00067;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctcgcaagcaccctatcaggca 22
          ||||||||||||||||||||||
Db     22 CTCGCAAGCACCCTATCAGGCA 1


RESULT  45
AAD25564
ID   AAD25564 standard; DNA; 23 BP.
XX
AC   AAD25564;
XX
DT   26-MAR-2002  (first entry)
XX
DE   HCV RNA 5' UTR amplifying PCR primer #2.
XX
KW   Hepatitis C virus; HCV; cytostatic; replication defective gene transfer;
KW   encapsidated RNA virus; gene therapy; cancer therapy; PCR primer; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200190302-A2.
XX
PD   29-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US15449.
XX
PR   24-MAY-2000; 2000US-206997P.
XX
PA   (FENG/) FENG Y.
PA   (TANG/) TANG H.
XX
PI   Feng Y,  Tang H;
XX
DR   WPI; 2002-066766/09.
XX
PT   Producing encapsidated RNA virus by coexpressing RNA virus genomic
PT   sequence linked to bacteriophage promoter, and coding sequence for
PT   bacteriophage polymerase linked to poxvirus promoter in eukaryotic cell
PT   cytoplasm  -
XX
PS   Example 1; Page 30; 49pp; English.
XX
CC   The patent discloses methods to produce RNA viral sequences, recombinant
CC   RNA viruses, mutants of RNA viruses and RNA virus-derived vectors in
CC   cell culture and in vitro using non-viable, replication defective helper
CC   vaccinia recombinants. These methods generate RNA viral genomes and viral
```

CC particles in cell culture and in vitro independent of their natural
CC replication pathways, bypassing the limitation of any cellular barriers.
CC The invention also relates to a method for producing encapsidated RNA
CC virus comprising coexpressing polypeptide coding sequences capable of
CC forming capsid and packaging RNA viral genomic sequence in eukaryotic
CC cell, a construct comprising RNA viral genomic sequence linked to
CC bacteriophage promoter and transcription terminator and bacteriophage
CC polymerase coding sequence, which is operably compatible with the
CC promoter and is linked to poxvirus promoter. The methods are useful
CC for producing infectious or non-infectious, replication-defective,
CC encapsidated RNA viruses such as hepatitis virus comprising an RNA
CC genome e.g. hepatitis C virus (HCV), immature hepatitis B virus or
CC hepatitis A virus, lentivirus, rhinovirus, influenza virus, LCMV,
CC arenavirus, parainfluenza virus, reovirus, rotavirus, astrovirus,
CC filovirus, or coronavirus. They are preferably useful for producing
CC encapsidated human immunodeficiency virus (HIV)-1, where the HIV-1
CC lacks a Rev-response element (RRE) or an envelope sequence. Methods
CC of the invention are also useful for producing replication defective
CC gene transfer and gene therapy vectors, particularly to transfer nucleic
CC acids to human cells in vivo and in vitro. The methods can be used for
CC packaging therapeutic sequences as gene therapy vector preparations that
CC are substantially free of helper virus and used as pharmaceuticals in
CC e.g. gene replacement therapy, or cancer therapy. The present DNA
CC sequence is a PCR primer which is used for amplifying the 5' untranslated
CC region (UTR) of HCV RNA.
XX
SQ Sequence 23 BP; 7 A; 9 C; 4 G; 3 T; 0 other;

Query Match 91.7%; Score 22; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||
Db      2 ctcgcaagcaccctatcaggca 23
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Search completed: August 26, 2002, 22:24:56
Job time: 6235 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 20:41:01 ; Search time 450.99 Seconds
(without alignments)
91.368 Million cell updates/sec

Title: US-10-037-990A-1
Perfect score: 24
Sequence: 1 gcagaaagcgtctagccatggcgt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 21

Total number of hits satisfying chosen parameters: 29

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

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17: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
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22: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	24	14	AAQ37573	HCV conserved regi
2	24	100.0	24	16	AAQ79964	Primer KY90 for HC
3	24	100.0	24	18	AAT64887	Hepatitis C virus
4	24	100.0	24	18	AAT93541	Sense primer KY80
5	24	100.0	24	18	AAT87096	HCV gene PCR prime
6	24	100.0	24	19	AAV18849	Primer KY80 for HC
7	24	100.0	24	19	AAV15320	Hepatitis C virus
8	24	100.0	24	20	AAZ23536	HCV wild type geno
9	24	100.0	24	20	AAZ09797	HCV PCR primer KY8
10	24	100.0	24	20	AAX78451	HCV PCR primer 1.
11	24	100.0	24	20	AAX23968	PCR primer KY80.
12	24	100.0	24	22	AAD19056	Hepatitis viral DN
13	24	100.0	24	22	AAH25403	PCR primer used to
14	24	100.0	26	14	AAQ37574	HCV conserved regi
15	24	100.0	26	18	AAT64888	Hepatitis C virus
16	24	100.0	26	18	AAT67193	Hepatitis C virus
17	24	100.0	26	19	AAV59058	Primer ST280A for
18	24	100.0	26	22	AAH25413	Forward PCR primer
19	24	100.0	77	22	AAS10490	HCV 5'-UTR domain
20	23	95.8	37	16	AAQ85920	Hepatitis C virus
21	23	95.8	37	16	AAQ75035	PCR primer for the
22	23	95.8	58	16	AAQ75033	Biotinylated oligo
23	21	87.5	21	14	AAQ52817	HCV target sequenc
24	21	87.5	21	19	AAV70448	HCV target DNA amp
c 25	21	87.5	21	21	AAA72990	Hepatitis C virus
26	21	87.5	21	22	AAH79078	HCV negative stran
27	21	87.5	21	24	ABA01127	HCV primer Outer F
28	21	87.5	24	22	AAH79081	HCV PCR primer SEQ
29	21	87.5	25	16	AAQ98291	Hepatitis C virus

ALIGNMENTS

RESULT 1
AAQ37573
ID AAQ37573 standard; DNA; 24 BP.
XX
AC AAQ37573;
XX
DT 23-JUN-1993 (first entry)
XX
DE HCV conserved region upstream primer/probe KY80, position 56-79.
XX
KW Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW regulation; US; Japan; C9; ss.
XX
OS Synthetic.
XX
PN EP529493-A.
XX
PD 03-MAR-1993.
XX
PF 19-AUG-1992; 92EP-0114115.
XX
PR 27-AUG-1991; 91US-0751305.
PR 21-JUL-1992; 92US-0918844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Resnick RM, Young KKY;
XX
DR WPI; 1993-068572/09.
XX
PT Compsn. comprising oligo:nucleotide probe-primer - used for
PT detecting hepatitis C virus strains Japan, US and C9
XX
PS Claim 4; Page 7; 43pp; English.
XX
CC The sequences given in AAQ37569-96 are oligonucleotides which can be
CC used as primers or probes which hybridise to the conserved region at
CC the 5'-end of the hepatitis C virus (HCV) genome. HCV is a small
CC RNA virus containing a small, positive sense, molecule of RNA about
CC 10,000 nucleotides in length. the genome contains a single, long,
CC open reading frame believed to translated in to a single, large
CC polyprotein and subsequently processed. The open reading frame
CC begins at nucleotide 343 (using the numbering system from the
CC prototype virus) following an untranslated region (UTR) the 5'UTR
CC sequence is relatively conserved and may be important in viral
CC replication and regulation. The 5' end of the coding region is also

```
CC   conserved.  These primer/probes can be used to identify different HCV
CC   isolates such as US, Japan and C9 (see also AAQ37597-601).
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 14;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT   2
AAQ79964
ID   AAQ79964 standard; DNA; 24 BP.
XX
AC   AAQ79964;
XX
DT   01-AUG-1995  (first entry)
XX
DE   Primer KY90 for HCV RNA.
XX
KW   Primer; PCR; polymerase chain reaction; amplification;
KW   RNA detection; reverse transcription; hepatitis C virus; HCV;
KW   ss.
XX
OS   Synthetic.
XX
PN   EP632134-A.
XX
PD   04-JAN-1995.
XX
PF   20-JUN-1994;   94EP-0109468.
XX
PR   01-JUL-1993;   93US-0086483.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Gelfand DH,  Myers TW,  Sigua CL;
XX
DR   WPI; 1995-037815/06.
XX
PT   Improved amplification method for target RNA - using buffering
PT   agent which buffers both pH and divalent cation concn.
XX
PS   Example 6; Page 22; 37pp; English.
XX
CC   The primers given in AAQ79963-64 were used to amplify HCV templates
CC   for use in a novel method of RNA amplification involving
CC   high-temp. reverse transcription and PCR.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 16;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT   3
AAT64887
ID   AAT64887 standard; DNA; 24 BP.
XX
AC   AAT64887;
XX
DT   12-MAR-1998  (first entry)
XX
DE   Hepatitis C virus (HCV) oligonucleotide KY80.
XX
KW   Hepatitis C virus; reverse transcription; probe; PCR primer;
KW   detection; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   EP787807-A2.
XX
PD   06-AUG-1997.
XX
PF   19-AUG-1992;   92EP-0065347.
XX
PR   21-JUL-1992;   92US-0918844.
PR   27-AUG-1991;   91US-0751305.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Resnick RM,  Young KKY;
XX
DR   WPI; 1997-387489/36.
XX
PT   Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT   nucleic acid - from many different strains without loss of
PT   specificity, allow single step reverse transcription and
PT   amplification
XX
PS   Claims 2 and 5; Page 7; 35pp; English.
XX
CC   This oligonucleotide KY80 can be used as a probe for detecting
CC   hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC   strain. This oligonucleotide can also be used as a primer for amplifying
CC   HCV nucleic acid. This primer is capable of amplifying HCV C9 prototype
CC   strains also. The sequence of this oligonucleotide is contained in a
CC   specific region of HCV genomic nucleic acid. The probe or the primer
CC   is preferably labelled. The probe is used to detect HCV nucleic acid,
CC   preferably after this has been amplified using the new primer in reverse
CC   transcription polymerase chain reaction (RT-PCR), for both diagnostic and
CC   epidemiological applications. The primer is effective for both reverse
CC   transcription and PCR, eliminating the need to open the reaction tube
CC   during the procedure. Amplification is effective (no need for a second
CC   round of PCR with nested primers) and provides high sensitivity.  The
CC   probe is directed to conserved regions and so can detect many different
CC   strains without loss of specificity.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match            100.0%;  Score 24;  DB 18;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT   4
AAT93541
ID   AAT93541 standard; DNA; 24 BP.
XX
AC   AAT93541;
XX
DT   19-FEB-1998  (first entry)
XX
DE   Sense primer KY80 for amplification of HCV RNA.
XX
KW   Armoured RNA; bacteriophage MS2; RT-PCR; ribonuclease; recombinant;
KW   Human Immunodeficiency virus; HIV; Hepatitis C Virus; HCV; viral RNA;
KW   detection; quantification standard; maturase protein; coat protein;
KW   PCR primer; QS RNA; reverse transcriptase-PCR; ss.
```

XX
OS Synthetic.
OS Hepatitis C Virus.
XX
PN US5677124-A.
XX
PD 14-OCT-1997.
XX
PF 03-JUL-1996; 96US-0675153.
XX
PR 03-JUL-1996; 96US-0675153.
XX
PA (AMBI-) AMBION INC.
PA (CENE-) CENETRON DIAGNOSTICS LLC.
XX
PI Dubois DB, Pasloske BL, Winkler MM;
XX
DR WPI; 1997-511866/47.
XX
PT Recombinant RNA segment encapsidated in bacteriophage viral coat
PT protein - RNA detection and/or quantification standard
XX
PS Example 5; Column 22; 23pp; English.
XX
CC This sense primer is used in the RT-PCR amplification of HCV RNA to
CC create a quantitative HCV "armoured RNA" standard. An "armoured RNA" is
CC a recombinant RNA segment encapsidated in bacteriophage viral coat
CC protein. The recombinant RNA segment comprises an operator coding
CC sequence, a viral maturase protein binding site, and a non-bacteriophage
CC sequence. The recombinant RNA in its packaged form is highly resistant to
CC ribonucleases, insuring that the RNA standard is not compromised by
CC inadvertent ribonuclease contamination. The armoured RNA standards are
CC ideal as RNA standards for the quantification of RNA viruses such as HIV
CC and HCV from human body fluids such as blood and cerebrospinal fluid.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatggcgt 24
||||||||||||||||||||||||
Db 1 gcagaaagcgtctagccatggcgt 24

RESULT 5
AAT87096
ID AAT87096 standard; DNA; 24 BP.
XX
AC AAT87096;
XX
DT 07-JAN-1998 (first entry)
XX
DE HCV gene PCR primer KY80.
XX
KW RNA; plasma; hepatitis C virus; HCV; primer; PCR;
KW polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN US5654179-A.
XX
PD 05-AUG-1997.
XX
PF 14-NOV-1990; 90US-0614921.
XX
PR 08-APR-1993; 93US-0044649.
PR 14-NOV-1990; 90US-0614921.
PR 19-JUN-1992; 92US-0901545.
PR 03-OCT-1994; 94US-0317220.
XX
PA (HYDS) HRI RES INC.
XX
PI Lin L;
XX
DR WPI; 1997-401849/37.
XX
PT Preparation of RNA samples from plasma - by alcohol precipitation
PT after lysis with guanidinium thiocyanate
XX
PS Disclosure; Column 47; 60pp; English.
XX
CC Primer KY80 (AAT87096) and primer KY78 (AAT87095) were used for the
CC PCR amplification of a 305 bp hepatitis C virus gene product (see
CC AAT87088). A claimed method for preparing RNA samples comprises: (a)
CC mixing plasma with an aqueous buffer solution containing guanidinium
CC thiocyanate and beta-mercaptoethanol; (b) heating the mixture; (c)
CC adding an equal volume of an alcohol to precipitate RNA; and (d)
CC recovering the RNA. The method can be used to prepare RNA samples
CC for subsequent amplification, especially for detecting pathogens,
CC e.g. hepatitis C virus or HIV. Compared with the known ''IsoQuick''
CC and ''RNAzol'' methods, the method uses fewer tubes (just one),
CC requires fewer steps, takes less time and produces no toxic waste.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatggcgt 24
||||||||||||||||||||||||
Db 1 gcagaaagcgtctagccatggcgt 24

RESULT 6
AAV18849
ID AAV18849 standard; DNA; 24 BP.
XX
AC AAV18849;
XX
DT 11-JUN-1998 (first entry)
XX
DE Primer KY80 for HCV DNA.
XX
KW PCR primer; HCV; nucleic acid standard; Armored RNA; ss.
XX
OS Synthetic.
OS Hepatitis virus.
XX
PN WO9800547-A1.
XX
PD 08-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US12551.
XX
PR 24-JUN-1997; 97US-0881571.
PR 03-JUL-1996; 96US-0021145.
PR 03-JUL-1996; 96US-0675153.
XX
PA (AMBI-) AMBION INC.
PA (CENE-) CENETRON DIAGNOSTICS LLC.
XX
PI Dubois DB, Pasloske BL, Winkler MM;
XX
DR WPI; 1998-086972/08.
XX
PT Ribonuclease resistant RNA molecules and their production - useful
PT as standards in quantitative PCR for pathogens, e.g HIV-1, HIV-2 and
PT HCV
XX
PS Example 5; Page 41; 134pp; English.
XX

```
CC   The present sequence is a primer for hepatitis C virus (HCV) DNA,
CC   which was used in the preparation of a nucleic acid standard,
CC   comprising a nuclease resistant nucleic acid segment encoding a
CC   standard nucleic acid, i.e. RNA. The ribonuclease resistant RNA
CC   standard, designated Armored RNA (RTM) is useful as an internal or
CC   external nucleic acid standard in quantitative assays, e.g. PCR or
CC   RT-PCR for the presence of a tested nucleic acid in blood samples.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 19;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT   7
AAV15320
ID   AAV15320 standard; DNA; 24 BP.
XX
AC   AAV15320;
XX
DT   28-MAY-1998  (first entry)
XX
DE   Hepatitis C virus PCR primer PKY80.
XX
KW   Hepatitis C virus; HCV; PCR primer; detection; reverse transcription;
KW   enzyme immunoassay; viral RNA; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   WO9746716-A1.
XX
PD   11-DEC-1997.
XX
PF   03-JUN-1997;   97WO-IT00128.
XX
PR   07-JUN-1996;   96IT-M000404.
XX
PA   (WESA ) WABCO BV.
XX
PI   Bosio P,  Clemenza F,  Strumia C;
XX
DR   WPI; 1998-042222/04.
XX
PT   Detection of hepatitis C virus - by reverse transcription,
PT   single-step PCR and detection by DNA enzyme immunoassay
XX
PS   Disclosure; Page 4; 26pp; English.
XX
CC   The present sequence represents a PCR primer involved in the method of
CC   the present invention for detecting hepatitis C virus (HCV). The method
CC   comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
CC   resulting cDNA by a single polymerase chain reaction in a reaction
CC   mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme
CC   unit; and (c) detecting the amplification product by DEIA (DNA enzyme
CC   immunoassay) using an oligonucleotide probe. The sensitivity of this
CC   method is at least equal to that achievable by more complicated assays
CC   using nested PCR.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 19;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT   8
AAZ23536
ID   AAZ23536 standard; DNA; 24 BP.
XX
AC   AAZ23536;
XX
DT   21-DEC-1999  (first entry)
XX
DE   HCV wild type genome primer KY80.
XX
KW   Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW   cellular; yeast; fungal; primer; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   DE19814828-A1.
XX
PD   07-OCT-1999.
XX
PF   02-APR-1998;   98DE-1014828.
XX
PR   02-APR-1998;   98DE-1014828.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Kessler C,  Haberhausen G,  Batz H,  Oerum H;
XX
DR   WPI; 1999-552286/47.
XX
PT   Nucleic acid amplification assay for detecting viral, bacterial,
PT   cellular, yeast or fungal nucleic acids  -
XX
PS   Example 1; Page 19; 28pp; German.
XX
CC   This invention describes a novel assay for a nucleic acid comprises:
CC   (a) generating amplification products from a fragment of the nucleic
CC   acid, (b) contacting the amplification products with a probe; and
CC   (c) detecting hybridization between the amplification product and the
CC   probe. The assay is useful for detection of viral, bacterial, cellular,
CC   yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
CC   or fungal samples, e.g. feces, smears, cell suspensions, cultures or
CC   tissue, cell or liquid biopsy samples. This sequence represents a
CC   primer used in the method of the invention.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT   9
AAZ09797
ID   AAZ09797 standard; DNA; 24 BP.
XX
AC   AAZ09797;
XX
DT   26-NOV-1999  (first entry)
XX
DE   HCV PCR primer KY80.
XX
KW   Probe; amplification; primer; reporter group; quencher group; PCR;
KW   amplicon; detection; ss.
```

```
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   DE19814001-A1.
XX
PD   30-SEP-1999.
XX
PF   28-MAR-1998;   98DE-1014001.
XX
PR   28-MAR-1998;   98DE-1014001.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Kessler C,  Haberhausen G,  Batz H,  Orum H;
XX
DR   WPI; 1999-552213/47.
XX
PT   Fluorescent nucleic acid amplification assay, useful for detection of
PT   viral, bacterial, cellular, yeast or fungal nucleic acids -
XX
PS   Example 1; Page 19; 16pp; German.
XX
CC   This invention describes a novel assay for a nucleic acid which comprises
CC   an amplification reaction using two non-overlapping primers, a polymerase
CC   with 5'-nuclease activity and a probe with reporter groups and quencher
CC   groups that binds a region other than that bound by the primers. The
CC   reaction generates products of less than 100 nucleotides. The assay is
CC   useful for detection of viral, bacterial, cellular, yeast or fungal
CC   nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC   samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC   or liquid biopsy samples. Compared with assays in which longer
CC   amplification products are generated, the assay can be performed more
CC   rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
CC   may be increased due to reduced competition between the short
CC   counterstrand of the amplicon and the detector probe. Specificity may
CC   also be increased because of the increased relative length of sequence B
CC   compared with the total length of the amplicon and the differentiability
CC   of subtypes may be increased. In addition signal-to-noise ratios may be
CC   increased with the new method because short amplicons have reduced
CC   potential for nonspecific hybridization. In addition reproducibility may
CC   be increased because small target regions on RNA genomes are less
CC   sensitive to RNA degradation, and the possibilities for secondary
CC   structure formation are reduced. This sequence represents a PCR primer
CC   used in the amplification of a region of HCV which is used to illustrate
CC   the method of the invention.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT  10
AAX78451
ID   AAX78451 standard; DNA; 24 BP.
XX
AC   AAX78451;
XX
DT   26-AUG-1999  (first entry)
XX
DE   HCV PCR primer 1.
XX
KW   RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
KW   ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV;
KW   HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   US5919625-A.
XX
PD   06-JUL-1999.
XX
PF   29-APR-1997;   97US-0841252.
XX
PR   03-JUL-1996;   96US-0675153.
PR   29-APR-1997;   97US-0841252.
XX
PA   (AMBI-) AMBION INC.
PA   (CENE-) CENETRON DIAGNOSTICS LLC.
XX
PI   Dubois DB,  Pasloske BL,  Winkler MM;
XX
DR   WPI; 1999-394617/33.
XX
PT   Ribonuclease resistant viral RNA standards
XX
PS   Example V; Column 31-32; 22pp; English.
XX
CC   This invention describes the construction of novel RNA standards for the
CC   quantification of human immunodeficiency virus (HIV) and hepatitis C
CC   virus (HCV) from e.g. cerebrospinal fluids. THe method involves (1)
CC   obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
CC   RNA standard, encapsulated in a bacteriophage viral coat protein, which
CC   comprises an RNA segment having a segment encoding a sequence that serves
CC   as a standard in detection or quantification of the RNA of interest;
CC   (3) mixing the sample with the standard; (4) isolating RNA from the
CC   mixture, and (5) assaying for the presence of the RNA. The method is
CC   useful for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1,
CC   HTLV-2, hepatitis G, an enterovirus, or a blood-borne pathogen. This
CC   sequence represents a PCR primer used to amplify a region of the
CC   Hepatitis C genome which is used in the method of the invention.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT  11
AAX23968
ID   AAX23968 standard; DNA; 24 BP.
XX
AC   AAX23968;
XX
DT   28-JUN-1999  (first entry)
XX
DE   PCR primer KY80.
XX
KW   Amplification; medical; forensic; diagnosis; food analysis; blood;
KW   environmental analysis; plant protection; veterinary medicine;
KW   human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia;
KW   screening; PCR primer; detection; probe; ss.
XX
OS   Synthetic.
XX
PN   DE19748690-A1.
XX
PD   06-MAY-1999.
XX
PF   04-NOV-1997;   97DE-1048690.
XX
PR   04-NOV-1997;   97DE-1048690.
```

XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
DR WPI; 1999-278780/24.
XX
PT Detecting nucleic acid by generating short amplicons and probing
PT e.g. for diagnosis, food and environmental analysis and plant
PT protection
XX
PS Example 1; Page 16; 22pp; German.
XX
CC This invention describes a method for the detection of nucleic acid
CC which comprises amplification and reaction of the amplicon with a probe.
CC The method is used to detect nucleic acid e.g. for medical or forensic
CC diagnosis, in food and environmental analysis, in plant protection and
CC veterinary medicine, e.g. for detecting human immune deficiency virus,
CC hepatitis B or C viruses, or Chlamydia, in blood screening. The method
CC provides target-dependent, exponential amplification for highly specific
CC and sensitive, reproducible and quantitative detection of one or more
CC nucleic acids (single or double stranded). The design of primers and
CC probes is sufficiently flexible to allow many nucleic acids to be
CC detected in a standardized reaction format using partly the same primers
CC and probes. Only small amplicons are produced (requiring short
CC amplification cycles), there is no competition/displacement between the
CC short counter-strand of the amplicon and the detection probe, and
CC specificity is high because the relative proportion of the internal
CC detection region is increased with respect to the total amplicon length,
CC allowing better differentiation between (viral) subtypes. Also short
CC amplicons are less likely to undergo non-specific hybridization, so
CC background is low, and short RNA sequences are more stable, with reduced
CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
CC PCR primers and probes used in the method of the invention.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatggcgt 24
||||||||||||||||||||||||
Db 1 gcagaaagcgtctagccatggcgt 24

RESULT 12
AAD19056
ID AAD19056 standard; DNA; 24 BP.
XX
AC AAD19056;
XX
DT 18-DEC-2001 (first entry)
XX
DE Hepatitis viral DNA amplifying forward PCR primer #30.
XX
KW Hepatitis virus; bacterial infection; fungi; protozoa; PCR primer;
KW amplification; blood-borne pathogen; sexually transmitted disease;
KW respiratory disease; ss.
XX
OS Hepatitis virus.
XX
PN WO200168921-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-US08110.
XX
PR 14-MAR-2000; 2000US-189344P.
XX
PA (INVE-) INVESTIGEN.
XX
PI Koshinsky H, Zwick MS, Mccue KF;
XX
DR WPI; 2001-611396/70.
XX
PT Simultaneous detection of biological entities such as bacteria, fungi
PT and viruses by specific nucleic acid amplification -
XX
PS Disclosure; Page 31; 55pp; English.
XX
CC The invention relates to a method and apparatus for the simultaneous
CC detection of multiple biological entities such as bacteria, fungi and
CC viruses by specific nucleic acid amplification. The invention also
CC relates to a kit for simultaneous detection of biological entities. The
CC kit is employed for detecting blood-borne pathogens, associated with a
CC variety of infectious diseases such as respiratory and sexually
CC transmitted diseases. The methods and apparatus are used for the
CC simultaneous detection of biological entities present in biological and
CC environment samples. In particular, they are used for monitoring diseases
CC cause by microorganisms associated with a respiratory or sexually
CC transmitted disease such as a bacterium (Staphylococcus, Pneumococcus,
CC Gonococcus, Haemophilus, Bacteroides, Escherichia or Salmonella), virus
CC (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV,
CC HDV, HEV, HGV or TTV), fungus (Aspergillus fumigatus, Blastomycosis,
CC dermatitis, Candida albicans) or protozoa (Entamoeba histolytica).
CC The present sequence is a PCR primer used for amplifying
CC Hepatitis viral DNA.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatggcgt 24
||||||||||||||||||||||||
Db 1 gcagaaagcgtctagccatggcgt 24

RESULT 13
AAH25403
ID AAH25403 standard; DNA; 24 BP.
XX
AC AAH25403;
XX
DT 22-AUG-2001 (first entry)
XX
DE PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-EP11459.
XX
PR 17-NOV-1999; 99EP-0122853.
PR 12-MAY-2000; 2000EP-0110165.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 2001-381247/40.
XX
PT Novel composition of magnetic glass particles for purification of DNA
PT or RNA in automated processes -
XX
PS Example 7; Page 94; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between

```
CC   5-500 nm. The composition is useful for the purification of nucleic
CC   acids. The composition can be used to process large quantities of
CC   nucleic acid samples, because it does not involve the particles being
CC   centrifuged or the fluids being drawn through glass fiber filters.
CC   PCR primers AAH25403-04 were used to amplify HCV DNA fragments. The
CC   amplified fragment can be purified using the method of the invention.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 22;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT  14
AAQ37574
ID   AAQ37574 standard; DNA; 26 BP.
XX
AC   AAQ37574;
XX
DT   23-JUN-1993  (first entry)
XX
DE   HCV conserved region upstream primer/probe KY144, position 54-79.
XX
KW   Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW   virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW   prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW   regulation; US; Japan; C9; ss.
XX
OS   Synthetic.
XX
PN   EP529493-A.
XX
PD   03-MAR-1993.
XX
PF   19-AUG-1992;   92EP-0114115.
XX
PR   27-AUG-1991;   91US-0751305.
PR   21-JUL-1992;   92US-0918844.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Resnick RM,  Young KKY;
XX
DR   WPI; 1993-068572/09.
XX
PT   Compsn. comprising oligo:nucleotide probe-primer - used for
PT   detecting hepatitis C virus strains Japan, US and C9
XX
PS   Claim 4; Page 7; 43pp; English.
XX
CC   The sequences given in AAQ37569-96 are oligonucleotides which can be
CC   used as primers or probes which hybridise to the conserved region at
CC   the 5'-end of the hepatitis C virus (HCV) genome.  HCV is a small
CC   RNA virus containing a small, positive sense, molecule of RNA about
CC   10,000 nucleotides in length.  the genome contains a single, long,
CC   open reading frame believed to translated in to a single, large
CC   polyprotein and subsequently processed.  The open reading frame
CC   begins at nucleotide 343 (using the numbering system from the
CC   prototype virus) following an untranslated region (UTR) the 5'UTR
CC   sequence is relatively conserved and may be important in viral
CC   replication and regulation.  The 5' end of the coding region is also
CC   conserved.  These primer/probes can be used to identify different HCV
CC   isolates such as US, Japan and C9 (see also AAQ37597-601).
XX
SQ   Sequence 26 BP; 7 A; 7 C; 8 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 14;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      3 gcagaaagcgtctagccatggcgt 26


RESULT  15
AAT64888
ID   AAT64888 standard; DNA; 26 BP.
XX
AC   AAT64888;
XX
DT   12-MAR-1998  (first entry)
XX
DE   Hepatitis C virus (HCV) oligonucleotide KY144.
XX
KW   Hepatitis C virus; reverse transcription; probe; PCR primer;
KW   detection; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   EP787807-A2.
XX
PD   06-AUG-1997.
XX
PF   19-AUG-1992;   92EP-0065347.
XX
PR   21-JUL-1992;   92US-0918844.
PR   27-AUG-1991;   91US-0751305.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Resnick RM,  Young KKY;
XX
DR   WPI; 1997-387489/36.
XX
PT   Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT   nucleic acid - from many different strains without loss of
PT   specificity, allow single step reverse transcription and
PT   amplification
XX
PS   Claims 2 and 5; Page 7; 35pp; English.
XX
CC   This oligonucleotide KY144 can be used as a probe for detecting
CC   hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC   strain. This oligonucleotide can also be used as a primer for amplifying
CC   HCV nucleic acid. This primer is  also capable of amplifying a HCV C9
CC   prototype strain. The sequence of this oligonucleotide is contained
CC   in a specific region of HCV genomic nucleic acid. The probe or the primer
CC   is preferably labelled. The probe is used to detect HCV nucleic acid,
CC   preferably after this has been amplified using the new primer in reverse
CC   transcription polymerase chain reaction (RT-PCR), for both diagnostic and
CC   epidemiological applications. The primer is effective for both reverse
CC   transcription and PCR, eliminating the need to open the reaction tube
CC   during the procedure. Amplification is effective (no need for a second
CC   round of PCR with nested primers) and provides high sensitivity.  The
CC   probe is directed to conserved regions and so can detect many different
CC   strains without loss of specificity.
XX
SQ   Sequence 26 BP; 7 A; 7 C; 8 G; 4 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 18;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      3 gcagaaagcgtctagccatggcgt 26
```

```
RESULT  16
AAT67193
ID   AAT67193 standard; DNA; 26 BP.
XX
AC   AAT67193;
XX
DT   13-FEB-1998  (first entry)
XX
DE   Hepatitis C virus (HCV) RNA amplification primer ST280A.
XX
KW   Hepatitis C virus; HCV; ST280A; reverse transcription PCR; RT-PCR;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   EP776981-A2.
XX
PD   04-JUN-1997.
XX
PF   21-NOV-1996;   96EP-0118704.
XX
PR   29-NOV-1995;   95US-0007739.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Tsang SY;
XX
DR   WPI; 1997-291296/27.
XX
PT   Oligonucleotide primers for hepatitis C virus RNA amplification  -
PT   by polymerase chain reaction
XX
PS   Claim 1; Page 11; 16pp; English.
XX
CC   This upstream primer ST280A is used in the amplification of the
CC   Hepatitis C virus (HCV) RNA by reverse transcription PCR. This is used
CC   to amplify a 250 base pair product from the 5' untranslated region of
CC   the HCV genome. This can be used to detect HCV in a sample with increased
CC   sensitivity. Amplification of HCV nucleic acid using this primer is up to
CC   100 times more efficient than amplification with prior art primers.
XX
SQ   Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 18;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT  17
AAV59058
ID   AAV59058 standard; DNA; 26 BP.
XX
AC   AAV59058;
XX
DT   07-JAN-1999  (first entry)
XX
DE   Primer ST280A for HCV fragment.
XX
KW   PCR primer; HCV; nucleic acid amplification; ss.
XX
OS   Synthetic.
OS   Human cytomegalovirus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   26
FT                   /*tag=  a
FT                   /note= "optionally benzylated, methylated, or
FT                          nitrobenzylated"
XX
PN   EP866071-A2.
XX
PD   23-SEP-1998.
XX
PF   12-MAR-1998;   98EP-0104461.
XX
PR   20-MAR-1997;   97US-0041127.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Will SG,  Young KKY;
XX
DR   WPI; 1998-482929/42.
XX
PT   Oligo-nucleotide(s) containing N-substituted nucleotide - useful as
PT   primers for nucleic acid amplification
XX
PS   Example 6; Page 16; 38pp; English.
XX
CC   This sequence represents a primer for a fragment of HCV, and is an
CC   example of an oligonucleotide of the invention. The oligonucleotides of
CC   the invention are of the formula 5'-S1-Nu-3' or 5'-S1-Nu-S2-3', where
CC   S1 is a sequence of 5-50 nucleotides; S2 is a sequence of 1-3
CC   nucleotides; and Nu is a nucleotide with a purine or pyrimidine base
CC   having an exocyclic amino group substituted by CHR1R2; R1, R2 are H,
CC   1-10C alkyl, alkoxy, optionally substituted phenyl, phenoxy or optionally
CC   substituted naphthyl. The oligonucleotides are useful as primers for
CC   nucleic acid amplification, preferably by polymerase chain reaction. Use
CC   of the modified primers reduces non-specific amplification, especially
CC   primer dimer formation, with a concomitant increase in the yield of the
CC   intended target.
XX
SQ   Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other;


  Query Match             100.0%;  Score 24;  DB 19;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT  18
AAH25413
ID   AAH25413 standard; DNA; 26 BP.
XX
AC   AAH25413;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Forward PCR primer used to amplify a HCV DNA fragment.
XX
KW   Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS   Hepatitis C virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   26
FT                   /*tag=  a
FT                   /note= "derivatisation with a p-(t-butyl)benzyl-residue"
XX
PN   WO200137291-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11459.
XX
PR   17-NOV-1999;   99EP-0122853.
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```
PR   12-MAY-2000; 2000EP-0110165.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Riedling M,  Geiger A;
XX
DR   WPI; 2001-381247/40.
XX
PT   Novel composition of magnetic glass particles for purification of DNA
PT   or RNA in automated processes -
XX
PS   Example 7; Page 98; 105pp; English.
XX
CC   The specification describes a composition of magnetic glass particles,
CC   which contain at least one magnetic object with a mean diameter between
CC   5-500 nm. The composition is useful for the purification of nucleic
CC   acids. The composition can be used to process large quantities of
CC   nucleic acid samples, because it does not involve the particles being
CC   centrifuged or the fluids being drawn through glass fiber filters.
CC   PCR primers AAH25413-14 were used to amplify HCV DNA fragments. The
CC   amplified fragment can be purified using the method of the invention.
XX
SQ   Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other;


  Query Match           100.0%;  Score 24;  DB 22;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 gcagaaagcgtctagccatggcgt 24


RESULT  19
AAS10490
ID   AAS10490 standard; RNA; 77 BP.
XX
AC   AAS10490;
XX
DT   24-OCT-2001  (first entry)
XX
DE   HCV 5'-UTR domain II EMSA RNA probe.
XX
KW   HCV 5'-UTR; minimal IRES; mIRES; internal ribosome entry site; eIF3;
KW   eukaryotic initiation factor 3; HCV translation initiation; antiviral;
KW   RNA electrophoretic gel mobility shift assay; EMSA; ss.
XX
OS   Hepatitis C virus strain Ia M67463.
XX
FH   Key             Location/Qualifiers
FT   misc_binding     1..5
FT                    /*tag=  a
FT                    /bound_moiety= "Forms double stranded region with
FT                                   bases 73-77"
FT   stem_loop        8..22
FT                    /*tag=  c
FT                    /note= "Designated as IIa"
FT   misc_binding     23..28
FT                    /*tag=  b
FT                    /bound_moiety= "Forms double stranded region with
FT                                   bases 60-55"
FT   stem_loop        32..50
FT                    /*tag=  c
FT                    /note= "Designated as IIb"
FT   misc_binding     55..60
FT                    /*tag=  d
FT                    /bound_moiety= "Forms double stranded region with
FT                                   bases 28-23"
FT   misc_binding     73..77
FT                    /*tag=  e
FT                    /bound_moiety= "Forms double stranded region with
FT                                   bases 5-1"
XX
PN   WO200144266-A2.
XX
PD   21-JUN-2001.
XX
PF   18-DEC-2000; 2000WO-GB04862.
XX
PR   16-DEC-1999;   99GB-0029820.
PR   22-DEC-1999;   99US-0171804.
XX
PA   (RIBO-) RIBOTARGETS LTD.
XX
PI   Karn J,  Walker S;
XX
DR   WPI; 2001-465050/50.
XX
PT   Nucleotide sequences derived from Hepatitis C virus, useful for
PT   identifying candidate antiviral compounds -
XX
PS   Disclosure; Fig 5E; 48pp; English.
XX
CC   The present sequence represents Hepatitis C virus (HCV) 5'-UTR
CC   domain II RNA probe used in a RNA electrophoretic gel mobility
CC   shift assay (EMSA). The present sequence is described in an
CC   invention relating to a novel compound comprising nucleotide sequences
CC   capable of annealing and which is derived from a 5'-untranslated
CC   region (UTR) of HCV which is essential for binding of eIF3 (eukaryotic
CC   initiation factor 3). The invention particularly relates to a
CC   sub-region of the HCV 5'-UTR referred to as the minimal internal
CC   ribosome entry site (mIRES) which can be used to identify drugs which
CC   inhibit HCV translation initiation. The compounds of the invention may
CC   be used to screen for potential HCV antiviral compounds. Assays based
CC   on the mIRES enable potential antivirals to be screened in a cheaper
CC   and easier way. It allows rapid assaying with a small volume of
CC   material and are suitable to parallel processing.
XX
SQ   Sequence 77 BP; 16 A; 20 C; 23 G; 18 U; 0 other;


  Query Match           100.0%;  Score 24;  DB 22;  Length 77;
  Best Local Similarity  83.3%;  Pred. No. 6.9e-05;
  Matches   20;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||:|:|||||:||||:
Db     26 gcagaaagcgucuagccauggcgu 49


RESULT  20
AAQ85920
ID   AAQ85920 standard; DNA; 37 BP.
XX
AC   AAQ85920;
XX
DT   02-NOV-1995  (first entry)
XX
DE   Hepatitis C virus genome internal PCR primer YK-103U.
XX
KW   Hepatitis C virus; HCV; non-A non-B; external PCR primer;
KW   YK-103U; primer specific detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature     1..13
FT                    /*tag=  a
FT                    /note= "oligo (dU) sequence"
XX
PN   WO9506753-A.
XX
PD   09-MAR-1995.
XX
PF   02-SEP-1994;   94WO-US09869.
```

XX
PR 03-SEP-1993; 93US-0116344.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI; 1995-115465/15.
XX
PT New method and kit for primer-specific detection of nucleic acids
PT - using two primers having a known sequence and a marker, resp
PT for solid-phase detection of amplification prods.
XX
PS Example 1; Page 12; 20pp; English.
XX
CC AAQ85918/19 are external, and AAQ85820/21 are internal PCR primers for
CC the Hepatitis C virus (HCV) genome. They were used to demonstrate
CC a new method for the primer specific detection of nucleic acids.
XX
SQ Sequence 37 BP; 6 A; 6 C; 7 G; 5 T; 0 other;

Query Match 95.8%; Score 23; DB 16; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 cagaaagcgtctagccatggcgt 24
||||||||||||||||||||||||
Db 14 cagaaagcgtctagccatggcgt 36

RESULT 21
AAQ75035
ID AAQ75035 standard; DNA; 37 BP.
XX
AC AAQ75035;
XX
DT 04-AUG-1995 (first entry)
XX
DE PCR primer for the amplification of a peptide-streptavidin-oligo.
XX
KW Synthetic peptide; solid phase immunoassay; ss.
XX
OS Synthetic.
XX
PN WO9426932-A.
XX
PD 24-NOV-1994.
XX
PF 13-MAY-1994; 94WO-US05407.
XX
PR 13-MAY-1993; 93US-0061694.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI; 1995-006819/01.
XX
PT Solid phase immunoassay using oligo:nucleotide as label - also
PT new conjugates of oligo:nucleotide coupled to antigenic peptide,
PT partic. for diagnosing hepatitis C or E virus infection
XX
PS Example; Page 19; 34pp; English.
XX
CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC They are used in a method for detecting an antigen in a subject. The
CC method involves binding the antigen to a solid support and then
CC reacting it with an immunoreactive ligand (L) bound to an oligo;
CC removing any unreacted L, and then detecting the presence of the
CC oligo. A similar method can be used to detect Abs, in which case the
CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as
CC the label allows Ag or Ab to be detected at very low levels. In the
CC example, anti-human antibodies are adsorbed on the surface of
CC microcentrifuge tubes and used to captrure antibodies from human
CC sera specimens. Then the tubes are incubated with a peptide-
CC streptavidin-oligo complex. After washing, PCR is performed, using
CC primers AAQ75034 and AAQ75035. AAQ75034 could be labelled with
CC another moiety, for example, biotin.
XX
SQ Sequence 37 BP; 6 A; 6 C; 7 G; 5 T; 13 U; 0 other;

Query Match 95.8%; Score 23; DB 16; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 cagaaagcgtctagccatggcgt 24
||||||||||||||||||||||||
Db 14 cagaaagcgtctagccatggcgt 36

RESULT 22
AAQ75033
ID AAQ75033 standard; DNA; 58 BP.
XX
AC AAQ75033;
XX
DT 04-AUG-1995 (first entry)
XX
DE Biotinylated oligonucleotide.
XX
KW Synthetic peptide; solid phase immunoassay; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1
FT /*tag= a
FT /note= "linked to biotin"
XX
PN WO9426932-A.
XX
PD 24-NOV-1994.
XX
PF 13-MAY-1994; 94WO-US05407.
XX
PR 13-MAY-1993; 93US-0061694.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI; 1995-006819/01.
XX
PT Solid phase immunoassay using oligo:nucleotide as label - also
PT new conjugates of oligo:nucleotide coupled to antigenic peptide,
PT partic. for diagnosing hepatitis C or E virus infection
XX
PS Example; Page 18; 34pp; English.
XX
CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC They are used in a method for detecting an antigen in a subject. The
CC method involves binding the antigen to a solid support and then
CC reacting it with an immunoreactive ligand (L) bound to an oligo;
CC removing any unreacted L, and then detecting the presence of the
CC oligo. A similar method can be used to detect Abs, in which case the
CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as
CC the label allows Ag or Ab to be detected at very low levels. In the
CC example, a synthetic peptide from the NS4 protein of the hepatitis
CC C virus with structure (AAR62943) is biotinylated using a
CC commercially available kit. A biotinylated oligo with the structure
CC 5'-biotinylated-AAQ75033-3' was prepd. This oligo is composed
CC of sequences of two PCR primers sepd. by a short additional
CC sequence. The shorter the region to be amplified the better the
CC efficiency of amplification obtd. The biotinylated oligo is pre-

```
CC   incubated with streptavidin. Then this complex linked by biotin-
CC   streptavidin binding. This INAA complex is then used in place of
CC   chemically prepd. oligo-peptide conjugates mentioned above.
XX
SQ   Sequence 58 BP; 10 A; 11 C; 15 G; 22 T; 0 other;


  Query Match             95.8%;  Score 23;  DB 16;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.00027;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 cagaaagcgtctagccatggcgt 24
          |||||||||||||||||||||||
Db     11 cagaaagcgtctagccatggcgt 33


RESULT  23
AAQ52817
ID   AAQ52817 standard; RNA; 21 BP.
XX
AC   AAQ52817;
XX
DT   26-MAY-1994  (first entry)
XX
DE   HCV target sequence 2.
XX
KW   RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
KW   picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KW   papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
KW   T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KW   influenza virus; HSV; herpes simplex virus; vector; immune response;
KW   antibody; ribozyme; viral RNA; treatment; ss.
XX
OS   Synthetic.
XX
PN   WO9323569-A.
XX
PD   25-NOV-1993.
XX
PF   29-APR-1993;   93WO-US04020.
XX
PR   11-MAY-1992;   92US-0882689.
PR   14-MAY-1992;   92US-0882712.
PR   14-MAY-1992;   92US-0882713.
PR   14-MAY-1992;   92US-0882714.
PR   14-MAY-1992;   92US-0882823.
PR   14-MAY-1992;   92US-0882824.
PR   14-MAY-1992;   92US-0882886.
PR   14-MAY-1992;   92US-0882888.
PR   14-MAY-1992;   92US-0882889.
PR   14-MAY-1992;   92US-0882921.
PR   14-MAY-1992;   92US-0883823.
PR   14-MAY-1992;   92US-0883849.
PR   14-MAY-1992;   92US-0884073.
PR   14-MAY-1992;   92US-0884074.
PR   14-MAY-1992;   92US-0884333.
PR   14-MAY-1992;   92US-0884422.
PR   14-MAY-1992;   92US-0884431.
PR   14-MAY-1992;   92US-0884436.
PR   14-MAY-1992;   92US-0884521.
PR   31-JUL-1992;   92US-0923738.
PR   26-AUG-1992;   92US-0936086.
PR   18-SEP-1992;   92US-0948359.
PR   15-OCT-1992;   92US-0963322.
PR   07-DEC-1992;   92US-0987129.
PR   07-DEC-1992;   92US-0987130.
PR   07-DEC-1992;   92US-0987133.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Draper KG,  Dudycz LW,  Holecek JJ,  Macejak DG,  Mamine JA;
PI   McSwiggen JA;
XX
DR   WPI; 1993-386599/48.
XX
PT   Enzymatic RNA molecules - used to inhibit viral replication,
PT   infection and gene expression
XX
PS   Claim 5; Fig 12; 287pp; English.
XX
CC   The sequences (AAQ52816-Q52823) are pref. hepatitus C virus target
CC   sequences for enzymatic RNA molecules. The RNA molecules are
CC   complementary to a substrate binding region in the specified gene
CC   target. They also have enzymatic activity, in that they specifically
CC   cleave RNA in the target. The ERMs interfere with viral replication and
CC   therefore have anti-viral properties. They can be used to attenuate
CC   viruses to be used in vaccines.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 7 G; 3 U; 0 other;


  Query Match             87.5%;  Score 21;  DB 14;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.004;
  Matches   18;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          ||||||||||:|:||||||:||
Db      1 gcagaaagcgucuagccaugg 21


RESULT  24
AAV70448
ID   AAV70448 standard; DNA; 21 BP.
XX
AC   AAV70448;
XX
DT   08-APR-1999  (first entry)
XX
DE   HCV target DNA amplifying 3' primer.
XX
KW   Nucleic acid detection; nucleic acid characterisation; hybridisation;
KW   infection; disease; cancer; forensic; paternity; multiplexing; HCV;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   WO9850403-A1.
XX
PD   12-NOV-1998.
XX
PF   05-MAY-1998;   98WO-US03194.
XX
PR   03-MAR-1998;   98US-0034205.
PR   05-MAY-1997;   97US-0851588.
PR   19-SEP-1997;   97US-0934097.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Anderson TA,  Brow MAD,  Dahlberg JE,  Dong F,  Fors L;
PI   Lyamichev VI,  Neri BP,  Prudent JR;
XX
DR   WPI; 1998-610317/51.
XX
PT   Detection and characterisation of nucleic acid sequences - by mixing
PT   a folded target and one or more probes to form a probe/folded target
PT   complex and detecting and characterising the complexes
XX
PS   Example 3; Page 116; 279pp; English.
XX
CC   The invention relates to methods and compositions of detection and
CC   characterisation of nucleic acid sequences and sequence changes. One
CC   method of detection and characterisation comprises: (a) providing: (i) a
CC   folded target having a DNA sequence comprising at least 1 double
CC   stranded region and at least 1 single stranded region; and (ii) at least
CC   1 probe complementary to at least a portion of the folded target; and
```

CC (b) mixing the target and probes so that the probe hybridises to form a
CC probe /folded target complex. Also provided are methods for determination
CC of structure formation in nucleic acid targets; for analysing folded
CC nucleic acids targets; and for analysis of nucleic acid structures. The
CC methods can be used for the detection and characterisation of nucleic
CC acid sequences to detect the presence of pathogenic nucleic acid
CC sequences indicative of an infection, the presence of variants or alleles
CC of mammalian genes associated with disease and cancers, and the
CC identification of the source of nucleic acids found in forensic samples,
CC as well as in paternity determinations. The methods allow simultaneous
CC analysis of both strands (e.g. the sense and antisense strands) and are
CC ideal for high-level multiplexing. The products produced are amenable to
CC qualitative, quantitative and positional analysis. The methods may be
CC performed in solution or in the solid phase (e.g. on a solid support).
CC The methods are powerful in that they allow for analysis of longer
CC fragments of nucleic acid than current methodologies. Sequences
CC AAV70447-48 represent primers used for the PCR amplification of hepatitis
CC c virus (HCV) target DNA used in the hybridisation analysis using
CC multiple capture probes for HCV genotyping.
XX
SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 other;

Query Match 87.5%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatgg 21
||||||||||||||||||||
Db 1 gcagaaagcgtctagccatgg 21

RESULT 25
AAA72990/c
ID AAA72990 standard; DNA; 21 BP.
XX
AC AAA72990;
XX
DT 24-NOV-2000 (first entry)
XX
DE Hepatitis C virus antisense oligonucleotide HCV88.
XX
KW Hepatitis C virus; HCV; antisense oligonucleotide; leuciferinase;
KW luciferase; HepG2; medicine; ss.
XX
OS Hepatitis C virus.
XX
PN CN1253138-A.
XX
PD 17-MAY-2000.
XX
PF 09-NOV-1998; 98CN-0124388.
XX
PR 09-NOV-1998; 98CN-0124388.
XX
PA (RADI-) RADIOMEDICINE ACAD MILITARY MEDICAL SCI.
XX
PI Wang S, Wang X, Zhu B;
XX
DR WPI; 2000-466526/41.
XX
PT Structure and usage of antisense oligonucleotide for treating diseases
PT correlative to hepatitis C virus -
XX
PS Claim 1; Page 1; 20pp; Chinese.
XX
CC The present invention describes antisense oligonucleotides which are
CC designed and synthesised on the basis of the gene structure of
CC hepatitis C virus (HCV) and can be used to suppress the expression of
CC HCV gene. The non-coding region 5' of HCV gene is used to regulate the
CC instantaneous expression system of leuciferinase gene in HepG2 cells
CC and the transgenic cell model HepG2.9706 of luciferase gene. The 15
CC antisense oligonucleotides (AAA72988 to AAA73002) which are complementary
CC to the non-coding region 5' and translational initiation region of HCV
CC are actively screened and evaluated to discover for the first time the
CC oligonucleotides HCV279, HCV349, HCV363, HCV65 and HCV 313 and their
CC chemical modified objects for suppressing the expression of HCV gene.
CC Thus, the present invention relates to the new medicine for treating the
CC diseases associated with HCV.
XX
SQ Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 other;

Query Match 87.5%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatgg 21
||||||||||||||||||||
Db 21 GCAGAAAGCGTCTAGCCATGG 1

RESULT 26
AAH79078
ID AAH79078 standard; DNA; 21 BP.
XX
AC AAH79078;
XX
DT 20-NOV-2001 (first entry)
XX
DE HCV negative strand RNA sense PCR primer.
XX
KW Transgenic animal model; human hepatotrophic pathogen; immunotherapy;
KW human hepatitis C virus; HCV; vaccine; antiviral; hyperlipidaemia;
KW atherosclerosis; PCR primer; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200167854-A1.
XX
PD 20-SEP-2001.
XX
PF 16-MAR-2001; 2001WO-CA00350.
XX
PR 17-MAR-2000; 2000US-0528120.
XX
PA (KNET/) KNETEMAN N M.
PA (TYRR/) TYRRELL D L.
PA (MERC/) MERCER D F.
XX
PI Kneteman NM, Tyrrell DL, Mercer DF;
XX
DR WPI; 2001-582368/65.
XX
PT New chimeric immunodeficient transgenic murine host susceptible to
PT hepatitis C virus infection, useful as model for screening compounds,
PT comprises chimeric liver, where transgene encodes urokinase-type
PT plasminogen activator -
XX
PS Example 4; Page 38; 78pp; English.
XX
CC The invention relates to a non-human animal model that is susceptible to
CC infection by human hepatotrophic pathogens, especially human hepatitis C
CC virus (HCV). The model is based on a non-human, immunocompromised
CC xenogeneic transgenic animal having a human-mouse chimeric liver. The
CC invention outlines the creation of a chimeric immunodeficient murine host
CC infected with human HCV and deficient in functional syngeneic B and T
CC lymphocytes, comprising a genomically integrated transgene encoding a
CC urokinase-type plasminogen activator in liver cells and a chimeric liver
CC comprising human hepatocytes engrafted into liver of the murine host,
CC where inoculation of chimeric host with HCV results in HCV infection. The
CC chimeric mouse model is useful for culturing human HCV, for screening
CC candidate agents for activity against a hepatotrophic pathogen,
CC especially a vaccine for active immunotherapy or for therapeutic
CC vaccination or an immunotherapeutic agent e.g. anti-HCV body or

```
CC   HCV-binding fragment, for evaluating liver toxicity of an agent, for the
CC   development of antiviral agents and also as animal model for
CC   hyperlipidaemic and atherosclerosis. The animal model provides the first
CC   instance of an animal that is susceptible to infection by HCV through the
CC   normal route of infection and further it can become more chronically,
CC   consistently and stably infected at viral titers that can be equated to
CC   viral titers in HCV-infected humans. The present sequence is that of a
CC   PCR primer for detection of negative-stranded HCV RNA.
XX
SQ   Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 other;


  Query Match             87.5%;  Score 21;  DB 22;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gaaagcgtctagccatggcgt 24
          |||||||||||||||||||||
Db      1 gaaagcgtctagccatggcgt 21


RESULT  27
ABA01127
ID   ABA01127 standard; DNA; 21 BP.
XX
AC   ABA01127;
XX
DT   06-FEB-2002  (first entry)
XX
DE   HCV primer Outer F.
XX
KW   Hepatitis C virus; HCV; nucleic acid synthesis;
KW   complementary chain synthesis; diagnosis; primer; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200177317-A1.
XX
PD   18-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-JP02771.
XX
PR   07-APR-2000; 2000JP-0111939.
XX
PA   (EIKE ) EIKEN KAGAKU KK.
XX
PI   Notomi T,  Nagamine K;
XX
DR   WPI; 2002-010907/01.
XX
PT   Isothermal amplification of nucleic acids using double-stranded nucleic
PT   acid as template to establish complementary chain synthesis reaction
PT   from primer enabling base pairing in domain to be annealed, useful e.g.
PT   in gene diagnosis -
XX
PS   Example 1; Page 41; 75pp; Japanese.
XX
CC   The invention relates to a method for synthesising a nucleic acid using
CC   a double-stranded nucleic acid as template and incubating under
CC   conditions allowing the establishment of a complementary chain synthesis
CC   reaction. The method uses an arbitrary primer to initiate the
CC   complementary chain synthesis reaction. The method is particularly
CC   useful in gene and disease diagnosis. It is a highly efficient and
CC   reaction specific method in which no temperature variation is required.
CC   The present sequence is a primer used in an example illustrating the
CC   invention.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 other;


  Query Match             87.5%;  Score 21;  DB 24;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 gcagaaagcgtctagccatgg 21


RESULT  28
AAH79081
ID   AAH79081 standard; DNA; 24 BP.
XX
AC   AAH79081;
XX
DT   20-NOV-2001  (first entry)
XX
DE   HCV PCR primer SEQ ID NO 5.
XX
KW   Transgenic animal model; human hepatotrophic pathogen; immunotherapy;
KW   human hepatitis C virus; HCV; vaccine; antiviral; hyperlipidaemia;
KW   atherosclerosis; PCR primer; ss.
XX
OS   Hepatitis C virus.
OS   Synthetic.
XX
PN   WO200167854-A1.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-CA00350.
XX
PR   17-MAR-2000; 2000US-0528120.
XX
PA   (KNET/) KNETEMAN N M.
PA   (TYRR/) TYRRELL D L.
PA   (MERC/) MERCER D F.
XX
PI   Kneteman NM,  Tyrrell DL,  Mercer DF;
XX
DR   WPI; 2001-582368/65.
XX
PT   New chimeric immunodeficient transgenic murine host susceptible to
PT   hepatitis C virus infection, useful as model for screening compounds,
PT   comprises chimeric liver, where transgene encodes urokinase-type
PT   plasminogen activator  -
XX
PS   Example 4; Page 39; 78pp; English.
XX
CC   The invention relates to a non-human animal model that is susceptible to
CC   infection by human hepatotrophic pathogens, especially human hepatitis C
CC   virus (HCV). The model is based on a non-human, immunocompromised
CC   xenogeneic transgenic animal having a human-mouse chimeric liver. The
CC   invention outlines the creation of a chimeric immunodeficient murine host
CC   infected with human HCV and deficient in functional syngeneic B and T
CC   lymphocytes, comprising a genomically integrated transgene encoding a
CC   urokinase-type plasminogen activator in liver cells and a chimeric liver
CC   comprising human hepatocytes engrafted into liver of the murine host,
CC   where inoculation of chimeric host with HCV results in HCV infection. The
CC   chimeric mouse model is useful for culturing human HCV, for screening
CC   candidate agents for activity against a hepatotrophic pathogen,
CC   especially a vaccine for active immunotherapy or for therapeutic
CC   vaccination or an immunotherapeutic agent e.g. anti-HCV body or
CC   HCV-binding fragment, for evaluating liver toxicity of an agent, for the
CC   development of antiviral agents and also as animal model for
CC   hyperlipidaemic and atherosclerosis. The animal model provides the first
CC   instance of an animal that is susceptible to infection by HCV through the
CC   normal route of infection and further it can become more chronically,
CC   consistently and stably infected at viral titers that can be equated to
CC   viral titers in HCV-infected humans. The present sequence is that of a
CC   PCR primer useful in a method for detection of negative-stranded HCV RNA
CC   by RNase protection assay.
XX
SQ   Sequence 24 BP; 6 A; 5 C; 8 G; 5 T; 0 other;
```

```
  Query Match             87.5%;  Score 21;  DB 22;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gaaagcgtctagccatggcgt 24
          |||||||||||||||||||||
Db      1 gaaagcgtctagccatggcgt 21


RESULT  29
AAQ98291
ID   AAQ98291 standard; DNA; 25 BP.
XX
AC   AAQ98291;
XX
DT   19-MAR-1996  (first entry)
XX
DE   Hepatitis C virus sense PCR detection primer P21.
XX
KW   Primer; hepatitis C virus; PCR; amplification; reverse transcription;
KW   detection; non-translated region; ss.
XX
OS   Synthetic.
XX
PN   JP07184695-A.
XX
PD   25-JUL-1995.
XX
PF   27-DEC-1993;   93JP-0332682.
XX
PR   27-DEC-1993;   93JP-0332682.
XX
PA   (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX
DR   WPI; 1995-287992/38.
XX
PT   Simple detection of Hepatitis C virus in a single reaction tube -
PT   useful for high sensitivity and ease of reproduction.
XX
PS   Example 3; Page 7; 14pp; Japanese.
XX
CC   The primers AAQ98270-94 are used in a novel simple method for the
CC   detection of hepatitis C virus.  The novel method involves the steps of
CC   extracting the virus from a sample, synthesising cDNA from the viral RNA
CC   by reverse transcription, amplifying the cDNA by a first PCR and
CC   reamplifying the amplified product in a second PCR, all of which occur in
CC   a single reaction tube.  The primers are designed based on a 334 bp
CC   sequence (AAQ98272) derived from a 5' non-translated region of the viral
CC   genome. This primer corresponds to bases 54-78 of AAQ98272.
XX
SQ   Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 other;


  Query Match             87.5%;  Score 21;  DB 16;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gaaagcgtctagccatggcgt 24
          |||||||||||||||||||||
Db      1 gaaagcgtctagccatggcgt 21


Search completed: August 26, 2002, 22:24:55
Job time: 6234 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 19:12:26 ; Search time 1915.63 Seconds
(without alignments)
262.178 Million cell updates/sec

Title: US-10-037-990A-1
Perfect score: 24
Sequence: 1 gcagaaagcgtctagccatggcgt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 25

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
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12: gb_sy:*
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14: gb_vi:*
15: em_ba:*
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17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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24: em_ph:*
25: em_pl:*
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29: em_vi:*
30: em_htg_hum:*
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32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	24	6	A68287	A68287 Sequence 8
2	24	100.0	24	6	AR054578	AR054578 Sequence
3	24	100.0	24	6	AX003941	AX003941 Sequence
4	24	100.0	24	6	AX021563	AX021563 Sequence
5	24	100.0	24	6	AX021622	AX021622 Sequence
6	24	100.0	24	6	AX147011	AX147011 Sequence
7	24	100.0	24	6	AX250664	AX250664 Sequence
8	24	100.0	24	6	I22146	I22146 Sequence 5
9	24	100.0	24	6	I26949	I26949 Sequence 17
10	24	100.0	24	6	I40301	I40301 Sequence 9
11	24	100.0	24	6	I59678	I59678 Sequence 9
12	24	100.0	24	6	I68634	I68634 Sequence 7
13	24	100.0	26	6	AR054575	AR054575 Sequence
14	24	100.0	26	6	AR094137	AR094137 Sequence
15	24	100.0	26	6	AX147021	AX147021 Sequence
16	24	100.0	26	6	I22147	I22147 Sequence 6
17	24	100.0	51	6	AX021612	AX021612 Sequence
18	24	100.0	77	6	AX172761	AX172761 Sequence
19	23	95.8	28	6	BD000263	BD000263 Oligonucl
20	21	87.5	21	6	AR131532	AR131532 Sequence
21	21	87.5	21	6	AR144109	AR144109 Sequence
22	21	87.5	21	6	AX250669	AX250669 Sequence
23	21	87.5	21	6	BD001049	BD001049 Method an
24	21	87.5	21	6	BD001478	BD001478 Method an
25	21	87.5	24	6	AX250672	AX250672 Sequence

ALIGNMENTS

RESULT 1
A68287
LOCUS A68287 24 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 8 from Patent WO9746716.
ACCESSION A68287
VERSION A68287.1 GI:4759408
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Bosio,P., Strumia,C. and Clemenza,F.
TITLE METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS
JOURNAL Patent: WO 9746716-A 8 11-DEC-1997;
WABCO B V (NL)
COMMENT Other publication IT RM960404 19971209.
FEATURES Location/Qualifiers
source 1. .24
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatggcgt 24
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Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 2
AR054578
LOCUS AR054578 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5837442.
ACCESSION AR054578
VERSION AR054578.1 GI:5980155
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

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REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tsang,S.Yen.
  TITLE     Oligonucleotide primers for amplifying HCV nucleic acid
  JOURNAL   Patent: US 5837442-A 4 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .24
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BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   3
AX003941
LOCUS       AX003941                  24 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9923249.
ACCESSION   AX003941
VERSION     AX003941.1  GI:9927601
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923249-A 1 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="KY80"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   4
AX021563
LOCUS       AX021563                  24 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9924606.
ACCESSION   AX021563
VERSION     AX021563.1  GI:10044847
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive nucleic acid detection method
  JOURNAL   Patent: WO 9924606-A 1 20-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .24
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                     /db_xref="taxon:11103"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 0.0018;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
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Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   5
AX021622
LOCUS       AX021622                  24 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9923250.
ACCESSION   AX021622
VERSION     AX021622.1  GI:10044905
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923250-A 1 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   6
AX147011
LOCUS       AX147011                  24 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 5 from Patent WO0137291.
ACCESSION   AX147011
VERSION     AX147011.1  GI:14346282
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Weindel,K., Riedling,M. and Geiger,A.
  TITLE     Magnetic glass particles, method for their preparation and uses
            thereof
  JOURNAL   Patent: WO 0137291-A 5 25-MAY-2001;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide primer (HCV forward)"
BASE COUNT        6 a      6 c      8 g      4 t
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  Query Match            100.0%;  Score 24;  DB 6;  Length 24;
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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   7
AX250664
LOCUS       AX250664                  24 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 60 from Patent WO0168921.
ACCESSION   AX250664
VERSION     AX250664.1  GI:15984408
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Koshinsky,H., Zwick,M.S. and Mccue,K.F.
  TITLE     Compositions and methods for simultaneous detection of multiple
            biological entities
  JOURNAL   Patent: WO 0168921-A 60 20-SEP-2001;
            Investigen (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="PCR Primer"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   8
I22146
LOCUS       I22146                    24 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 5 from patent US 5527669.
ACCESSION   I22146
VERSION     I22146.1  GI:1602500
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Resnick,R.M. and Young,K.K.Y.
  TITLE     Methods, primers and probes for detection of hepatitis C and novel
            variants
  JOURNAL   Patent: US 5527669-A 5 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 0.0018;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT   9
I26949
LOCUS       I26949                    24 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 17 from patent US 5561058.
ACCESSION   I26949
VERSION     I26949.1  GI:1606819
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Gelfand,D.H., Myers,T.W. and Sigua,C.L.
  TITLE     Methods for coupled high temperatures reverse transcription and
            polymerase chain reactions
  JOURNAL   Patent: US 5561058-A 17 01-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  10
I40301
LOCUS       I40301                    24 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 9 from patent US 5620852.
ACCESSION   I40301
VERSION     I40301.1  GI:2082593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Lin,L., Cimino,G. and Zhu,Y.S.
  TITLE     Nucleic acid preparation methods
  JOURNAL   Patent: US 5620852-A 9 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 0.0018;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  11
I59678
LOCUS       I59678                    24 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 9 from patent US 5654179.
ACCESSION   I59678
VERSION     I59678.1  GI:2478310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 24)
  AUTHORS   Lin,L.
  TITLE     Nucleic acid preparation methods
  JOURNAL   Patent: US 5654179-A 9 05-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


  Query Match             100.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  12
I68634
LOCUS       I68634                   24 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 7 from patent US 5677124.
ACCESSION   I68634
VERSION     I68634.1  GI:2830756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   DuBois,D.B., Winkler,M.M. and Pasloske,B.L.
  TITLE     Ribonuclease resistant viral RNA standards
  JOURNAL   Patent: US 5677124-A 7 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      6 c      8 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  13
AR054575
LOCUS       AR054575                 26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5837442.
ACCESSION   AR054575
VERSION     AR054575.1  GI:5980152
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Tsang,S.Yen.
  TITLE     Oligonucleotide primers for amplifying HCV nucleic acid
  JOURNAL   Patent: US 5837442-A 1 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        7 a      6 c      8 g      5 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
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Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  14
AR094137
LOCUS       AR094137                 26 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 3 from patent US 6001611.
ACCESSION   AR094137
VERSION     AR094137.1  GI:10020882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Will,S.Gordon.
  TITLE     Modified nucleic acid amplification primers
  JOURNAL   Patent: US 6001611-A 3 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        7 a      6 c      8 g      5 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
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Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24


RESULT  15
AX147021
LOCUS       AX147021                 26 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 15 from Patent WO0137291.
ACCESSION   AX147021
VERSION     AX147021.1  GI:14346292
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Weindel,K., Riedling,M. and Geiger,A.
  TITLE     Magnetic glass particles, method for their preparation and uses
            thereof
  JOURNAL   Patent: WO 0137291-A 15 25-MAY-2001;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .26
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                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide primer (HCV forward)"
     modified_base   26
                     /note="derivatization with a p-(t-butyl)benzyl-residue"
                     /mod_base=OTHER
BASE COUNT        7 a      6 c      8 g      5 t
ORIGIN


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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGGCGT 24
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RESULT  16
I22147
LOCUS       I22147                    26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 6 from patent US 5527669.
ACCESSION   I22147
VERSION     I22147.1  GI:1602501
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Resnick,R.M. and Young,K.K.Y.
  TITLE     Methods, primers and probes for detection of hepatitis C and novel
            variants
  JOURNAL   Patent: US 5527669-A 6 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        7 a      7 c      8 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.0018;
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Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      3 GCAGAAAGCGTCTAGCCATGGCGT 26


RESULT  17
AX021612
LOCUS       AX021612                  51 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 50 from Patent WO9924606.
ACCESSION   AX021612
VERSION     AX021612.1  GI:10044896
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive nucleic acid detection method
  JOURNAL   Patent: WO 9924606-A 50 20-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT       11 a     12 c     15 g     13 t
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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db      8 GCAGAAAGCGTCTAGCCATGGCGT 31


RESULT  18
AX172761
LOCUS       AX172761                  77 bp    mRNA    linear   PAT 03-JUL-2001
DEFINITION  Sequence 9 from Patent WO0144266.
ACCESSION   AX172761
VERSION     AX172761.1  GI:14597857
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 77)
  AUTHORS   Karn,J.C. and Walker,S.C.
  TITLE     Nucleic acid compounds and screening assays using the same
  JOURNAL   Patent: WO 0144266-A 9 21-JUN-2001;
            RiboTargets Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .77
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Probe"
BASE COUNT       16 a     20 c     23 g     18 t
ORIGIN


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Qy      1 gcagaaagcgtctagccatggcgt 24
          ||||||||||||||||||||||||
Db     26 GCAGAAAGCGTCTAGCCATGGCGT 49


RESULT  19
BD000263
LOCUS       BD000263                  28 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Oligonucleotide primers for efficient detection of hepatitis C
            virus (HCV) and methods of use thereof.
ACCESSION   BD000263
VERSION     BD000263.1  GI:18623342
KEYWORDS    JP 2000279200-A/1.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Lynen,J.M. and Gorman,K.M.
  TITLE     Oligonucleotide primers for efficient detection of hepatitis C
            virus (HCV) and methods of use thereof
  JOURNAL   Patent: JP 2000279200-A 1 10-OCT-2000;
            ORTHO CLINICAL DIAGNOSTICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000279200-A/1
            PD   10-OCT-2000
            PF   03-FEB-2000 JP 2000032656
            PR   03-FEB-1999 US    60/118497
            PI   JEFFREY M LYNEN,KEVIN M GORMAN
            PC   C12Q1/68,C12N15/09//(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
            PC   C12R1:92)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .28
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      6 c      8 g      6 t
ORIGIN


  Query Match             95.8%;  Score 23;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.0069;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 cagaaagcgtctagccatggcgt 24
          |||||||||||||||||||||||
Db      1 CAGAAAGCGTCTAGCCATGGCGT 23


RESULT  20
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AR131532
LOCUS       AR131532                 21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 25 from patent US 6194149.
ACCESSION   AR131532
VERSION     AR131532.1  GI:14120435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Neri,B., Dong,F., Lyamichev,V., Brow,M.AnnD. and Fors,L.
  TITLE     Target-dependent reactions using structure-bridging
            oligonucleotides
  JOURNAL   Patent: US 6194149-A 25 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        6 a      5 c      7 g      3 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 0.11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21


RESULT  21
AR144109
LOCUS       AR144109                 21 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 25 from patent US 6210880.
ACCESSION   AR144109
VERSION     AR144109.1  GI:15105976
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lyamichev,V.I., Dong,F., Brow,M.AnnD., Fors,L. and Neri,B.P.
  TITLE     Polymorphism analysis by nucleic acid structure probing with
            structure-bridging oligonucleotides
  JOURNAL   Patent: US 6210880-A 25 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        6 a      5 c      7 g      3 t
ORIGIN


  Query Match            87.5%;  Score 21;  DB 6;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0.11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21


RESULT  22
AX250669
LOCUS       AX250669                 21 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 2 from Patent WO0167854.
ACCESSION   AX250669
VERSION     AX250669.1  GI:15984413
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kneteman,N.M., Tyrrell,L.D. and Mercer,D.F.
  TITLE     Chimeric animal model susceptible to human hepatitis c virus
            infection
  JOURNAL   Patent: WO 0167854-A 2 20-SEP-2001;
            Kneteman, Norman M. (CA) ; Tyrrell, Lorne D. (CA) ; Mercer, David
            F. (CA)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        5 a      5 c      7 g      4 t
ORIGIN


  Query Match            87.5%;  Score 21;  DB 6;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0.11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gaaagcgtctagccatggcgt 24
          |||||||||||||||||||||
Db      1 GAAAGCGTCTAGCCATGGCGT 21


RESULT  23
BD001049
LOCUS       BD001049                 21 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001049
VERSION     BD001049.1  GI:18625608
KEYWORDS    JP 2000342285-A/209.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342285-A 209 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342285-A/209
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132616
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
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            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      5 c      7 g      3 t
ORIGIN
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  Query Match            87.5%;  Score 21;  DB 6;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0.11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21


RESULT  24
BD001478
LOCUS       BD001478                  21 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001478
VERSION     BD001478.1  GI:18626037
KEYWORDS    JP 2000342286-A/209.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342286-A 209 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342286-A/209
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132651
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
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            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
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            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
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            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
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            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
            PC   A61K39/135,
            PC   A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
            PC   A61P1/16,
            PC   A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
              (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
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            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      5 c      7 g      3 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 0.11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gcagaaagcgtctagccatgg 21
          |||||||||||||||||||||
Db      1 GCAGAAAGCGTCTAGCCATGG 21


RESULT  25
AX250672
LOCUS       AX250672                  24 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0167854.
ACCESSION   AX250672
VERSION     AX250672.1  GI:15984416
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kneteman,N.M., Tyrrell,L.D. and Mercer,D.F.
  TITLE     Chimeric animal model susceptible to human hepatitis c virus
            infection
  JOURNAL   Patent: WO 0167854-A 5 20-SEP-2001;
            Kneteman, Norman M. (CA) ; Tyrrell, Lorne D. (CA) ; Mercer, David
            F. (CA)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        6 a      5 c      8 g      5 t
ORIGIN


  Query Match            87.5%;  Score 21;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 0.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 gaaagcgtctagccatggcgt 24
          |||||||||||||||||||||
Db      1 GAAAGCGTCTAGCCATGGCGT 21


Search completed: August 26, 2002, 21:20:52
Job time: 7706 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 19:44:36 ; Search time 3233.25 Seconds
(without alignments)
100.186 Million cell updates/sec

Title: US-10-037-990A-1
Perfect score: 24
Sequence: 1 gcagaaagcgtctagccatggcgt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:14:58 ; Search time 3233.25 Seconds
(without alignments)
87.663 Million cell updates/sec

Title: US-10-037-990A-3
Perfect score: 21
Sequence: 1 gtcgtgcagcctccaggaccc 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : EST:*
1: em_estba:*
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3: em_estin:*
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5: em_estov:*
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10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
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15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:17:12 ; Search time 119.4 Seconds
(without alignments)
43.202 Million cell updates/sec

Title: US-10-037-990A-3
Perfect score: 21
Sequence: 1 gtcgtgcagcctccaggaccc 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: August 26, 2002, 22:17:12
Job time: 5905 sec

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            PC   C12Q1/68,C12N15/09//(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
            PC   C12R1:92)
            CC
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
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ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.041;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     21 GTCGTGCAGCCTCCAGGACCC 1


RESULT   3
AX003946
LOCUS       AX003946                 48 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 6 from Patent WO9923249.
ACCESSION   AX003946
VERSION     AX003946.1  GI:9927606
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C. and Bartl,K.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923249-A 6 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT        9 a      18 c     14 g      7 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 6;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 0.039;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     10 GTCGTGCAGCCTCCAGGACCC 30


RESULT   4
AX003947
LOCUS       AX003947                 48 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 7 from Patent WO9923249.
ACCESSION   AX003947
VERSION     AX003947.1  GI:9927607
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C. and Bartl,K.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923249-A 7 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE)
FEATURES             Location/Qualifiers
     source          1. .48
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                     /db_xref="taxon:9606"
BASE COUNT        9 a      17 c     14 g      8 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 6;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 0.039;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     10 GTCGTGCAGCCTCCAGGACCC 30


RESULT   5
AX021565
LOCUS       AX021565                 48 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9924606.
ACCESSION   AX021565
VERSION     AX021565.1  GI:10044849
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive nucleic acid detection method
  JOURNAL   Patent: WO 9924606-A 3 20-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT        9 a      18 c     14 g      7 t
ORIGIN


  Query Match             100.0%;  Score 21;  DB 6;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 0.039;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtcgtgcagcctccaggaccc 21
          |||||||||||||||||||||
Db     10 GTCGTGCAGCCTCCAGGACCC 30


RESULT   6
AX021566
LOCUS       AX021566                 48 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9924606.
ACCESSION   AX021566
VERSION     AX021566.1  GI:10044850
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive nucleic acid detection method
  JOURNAL   Patent: WO 9924606-A 4 20-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 21:20:54 ; Search time 1915.63 Seconds
(without alignments)
229.406 Million cell updates/sec

Title: US-10-037-990A-3
Perfect score: 21
Sequence: 1 gtcgtgcagcctccaggaccc 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	6	AX147016	AX147016 Sequence
c 2	21	100.0	27	6	BD000273	BD000273 Oligonucl
3	21	100.0	48	6	AX003946	AX003946 Sequence
4	21	100.0	48	6	AX003947	AX003947 Sequence
5	21	100.0	48	6	AX021565	AX021565 Sequence
6	21	100.0	48	6	AX021566	AX021566 Sequence
7	21	100.0	48	6	AX021575	AX021575 Sequence
8	21	100.0	48	6	AX021576	AX021576 Sequence
9	21	100.0	48	6	AX021631	AX021631 Sequence
10	21	100.0	48	6	AX021632	AX021632 Sequence

ALIGNMENTS

RESULT 1
AX147016
LOCUS AX147016 21 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 10 from Patent WO0137291.
ACCESSION AX147016
VERSION AX147016.1 GI:14346287
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 21)
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses thereof
JOURNAL Patent: WO 0137291-A 10 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
source 1. .21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide probe (HCV)"
modified_base 1
/note="Ruthenium3+-(tris-bipyridyl)-derivatisation"
/mod_base=OTHER
BASE COUNT 3 a 9 c 6 g 3 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagcctccaggaccc 21
||||||||||||||||||||
Db 1 GTCGTGCAGCCTCCAGGACCC 21

RESULT 2
BD000273/c
LOCUS BD000273 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD000273
VERSION BD000273.1 GI:18623352
KEYWORDS JP 2000279200-A/11.
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 11 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT OS Artificial Sequence
PN JP 2000279200-A/11
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656